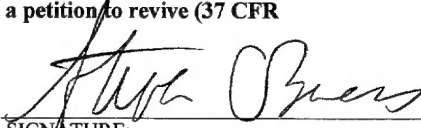


28 RECEIVED 27 JAN 1998

49/000004

FORM PTO-1390 (REV 10-94)		U S DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE	ATTORNEY'S DOCKET NUMBER
TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C. 371			600.314USWO
INTERNATIONAL APPLICATION NO. PCT/US96/12067			U S APPLICATION NO (If known, see 37 CFR 1.5) PRIORITY DATE CLAIMED 21 July 1995 (21.07.95)
INTERNATIONAL FILING DATE 19 July 1996 (19.07.96)			
TITLE OF INVENTION ANALYSIS OF ALPHA INTEGRINS FOR THE DIAGNOSIS OF DIABETIC NEPHROPATHY			
APPLICANT(S) FOR DO/EO/US TSILIBARY, Photini-Effe; ³⁻⁰³ CHARONIS, Aristidis, S.; ⁴⁻⁰³ SETTY, Suman; and MAUER, Michael			
Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:			
1. <input checked="" type="checkbox"/> This is a FIRST submission of items concerning a filing under 35 U.S.C. 371.			
2. <input type="checkbox"/> This is a SECOND or SUBSEQUENT submission of items concerning a filing under 35 U.S.C. 371.			
3. <input type="checkbox"/> This express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39(1).			
4. <input type="checkbox"/> A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.			
5. <input checked="" type="checkbox"/> A copy of the International Application as filed (35 U.S.C. 371(c)(2))			
a. <input type="checkbox"/> is transmitted herewith (required only if not transmitted by the International Bureau).			
b. <input type="checkbox"/> has been transmitted by the International Bureau.			
c. <input checked="" type="checkbox"/> is not required, as the application was filed in the United States Receiving Office (RO/US)			
6. <input type="checkbox"/> A translation of the International Application into English (35 U.S.C. 371(c)(2)).			
7. <input checked="" type="checkbox"/> Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3))			
a. <input type="checkbox"/> are transmitted herewith (required only if not transmitted by the International Bureau).			
b. <input type="checkbox"/> have been transmitted by the International Bureau.			
c. <input type="checkbox"/> have not been made; however, the time limit for making such amendments has NOT expired.			
d. <input checked="" type="checkbox"/> have not been made and will not be made.			
8. <input type="checkbox"/> A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).			
9. <input type="checkbox"/> An oath or declaration of the inventor(s) (35 U.S.C. 371 (c)(4)).			
10. <input type="checkbox"/> A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).			
Items 11. to 16. below concern document(s) or information included:			
11. <input type="checkbox"/> An Information Disclosure Statement under 37 CFR 1.97 and 1.98.			
12. <input type="checkbox"/> An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.			
13. <input type="checkbox"/> A FIRST preliminary amendment.			
<input type="checkbox"/> A SECOND or SUBSEQUENT preliminary amendment.			
14. <input type="checkbox"/> A substitute specification.			
15. <input type="checkbox"/> A change of power of attorney and/or address letter.			
16. <input type="checkbox"/> Other items or information:			

U.S. APPLICATION NO (If known, see 37 CFR 1.5)X		INTERNATIONAL APPLICATION NO PCT/US96/12067		ATTORNEY'S DOCKET NUMBER 600.314USWO	
17. x The following fees are submitted:				CALCULATIONS PTO USE ONLY	
BASIC NATIONAL FEE (37 CFR 1.492(a) (1)-(5)):					
Search Report has been prepared by the EPO or JPO.....\$930.00					
International preliminary examination fee paid to USPTO (37 CFR 1.482)\$720.00					
No international preliminary examination fee paid to USPTO (37 CFR 1.482) but international search fee paid to USPTO (37 CFR 1.445(a)(2))\$790.00					
Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO \$1070.00					
International preliminary examination fee paid to USPTO (37 CFR 1.482) and all claims satisfied provisions of PCT Article 33(2)-(4)\$98.00					
ENTER APPROPRIATE BASIC FEE AMOUNT =				\$1070.00	
Surcharge of \$130.00 for furnishing the oath or declaration later than [] 20 [] 30 months from the earliest claimed priority date (37 CFR 1.492(e)).				\$	
CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE		
Total claims	30 -20 = 10		X \$22.00	\$ 220.00	
Independent claims	4 -3 = 1		X \$82.00	\$ 82.00	
MULTIPLE DEPENDENT CLAIM(S) (if applicable)			+ \$250.00	\$	
TOTAL OF ABOVE CALCULATIONS =				\$1372.00	
Reduction by 1/2 for filing by small entity, if applicable. Verified Small Entity Statement must also be filed (Note 37 CFR 1.9, 1.27, 1.28).				\$	
SUBTOTAL =				\$1372.00	
Processing fee of \$130.00 for furnishing the English translation later than [] 20 [] 30 months from the earliest claimed priority date (37 CFR 1.492(f)).				+ \$	
TOTAL NATIONAL FEE =				\$1372.00	
Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). \$40.00 per property				+ \$	
TOTAL FEES ENCLOSED =				\$1372.00	
				Amount to be:	
				refunded	\$
				charged	\$
a. X A check in the amount of \$1284.90 \$1372.00 to cover the above fees is enclosed.					
b. [] Please charge my Deposit Account No. _____ in the amount of \$ _____ to cover the above fees. A duplicate copy of this sheet is enclosed.					
c. X The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. 13-2725. A duplicate copy of this sheet is enclosed.					
NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status.					
				 SIGNATURE:	
SEND ALL CORRESPONDENCE TO: Denise M. Kettelberger MERCHANT, GOULD, SMITH, EDELL, WELTER & SCHMIDT, P.A. 3100 Norwest Center 90 South Seventh Street 3100 Norwest Center Minneapolis, Minnesota 55402				Steven C. Bruess NAME 34,130 REGISTRATION NUMBER	

S/N 09/000,004

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant: TSILIBARY, ET AL. Examiner: UNKNOWN
Serial No.: 09/000,004 Group Art Unit: UNKNOWN
Filed: JANUARY 21, 1998 Docket No.: 600.314USWO
Title: ANALYSIS OF ALPHA INTEGRINS FOR THE DIAGNOSIS OF DIABETIC
NEPHROPATHY

CERTIFICATE UNDER 37 CFR 1.8: The undersigned hereby certifies that this correspondence is being deposited in the United States Postal Service, as first class mail, with sufficient postage, in an envelope addressed to: BOX PCT, Commissioner for Patents, Washington, D.C. 20231 on May 23, 2001.

By: Anne Harrison
Name: Anne Harrison

PRELIMINARY AMENDMENT

BOX PCT
Commissioner for Patents
Washington, D.C. 20231

Dear Sir:

IN THE ABSTRACT

Please insert the attached Abstract into the specification of the application as the last page thereof.

IN THE SPECIFICATION

Page 1, after the title, please insert the following paragraph:

--This application is a Nonprovisional of U.S. Provisional Application No. 60/001,387 filed on July 21, 1995; U.S. Provisional Application No. 60/001,861 filed on August 3, 1995; and U.S. Provisional Application No. 60/016,700 filed May 2, 1996.--

IN THE CLAIMS

Please cancel claim 1-30 and enter new claims 31-56.

31. (NEW) A method for identifying a mammal having or at risk for developing glomerulonephropathy comprising the steps of:

analyzing integrin subunit expression in a mammalian tissue sample known to contain cells expressing $\alpha 1$ and $\alpha 2$ integrin subunits and in a control tissue sample; and correlating a decreased level of $\alpha 1$ integrin subunit expression or an increased level of $\alpha 2$ integrin subunit expression in the sample tissue as compared with the control tissue with the presence of or risk of developing nephropathy.

32. (NEW) A method for identifying a mammal having or at risk for developing glomerulonephropathy comprising the steps of:

analyzing integrin subunit expression in a mammalian tissue sample known to contain cells expressing $\alpha 1$ and $\alpha 2$ integrin subunits and in a control tissue sample; and correlating a decreased level of $\alpha 1$ integrin subunit expression and an increased level of $\alpha 2$ integrin subunit expression in the sample tissue as compared with the control tissue with the presence of or risk of developing nephropathy.

33. (NEW) The method of claim 31, wherein the mammal is a human.

34. (NEW) The method of claim 31, wherein the tissue sample is a kidney biopsy, a skin biopsy, or blood.

35. (NEW) The method of claim 31, wherein said analyzing comprises *in situ* hybridization.

36. (NEW) The method of claim 35, wherein said *in situ* hybridization comprises PCR enhanced *in situ* hybridization.

37. (NEW) The method of claim 31, wherein said analyzing comprises isolating RNA from the sample.

46. (NEW) The method of claim 31, wherein a decrease of about 25% - 100% in the level of $\alpha 1$ integrin subunit expression in the sample tissue as compared with the control is correlated with nephropathy.

47. (NEW) A method for identifying a mammal having diabetes who has or is at risk for developing secondary pathological changes associated with diabetes comprising the steps of:
analyzing integrin subunit expression in a mammalian tissue sample known to contain cells expressing $\alpha 1$ and $\alpha 2$ integrin subunits and in a control tissue sample; and
correlating a decreased level of $\alpha 1$ integrin subunit expression and/or an increased level of $\alpha 2$ integrin subunit expression in the sample tissue as compared with the control tissue with the presence of or risk of developing secondary pathological changes associated with diabetes.

48. (NEW) A kit for the diagnosis of nephropathy comprising:
a set of hybridization probes or antibodies capable of detecting each of $\alpha 1$ and $\alpha 2$ integrin subunit expression in a tissue sample.

49. (NEW) The kit of claim 48, further comprising nucleic acid primer pairs for amplification of $\alpha 1$ and $\alpha 2$ integrin subunits.

50. (NEW) The kit of claim 48, comprising one or more of the following primers for amplification of $\alpha 1$: Sequence ID Nos. 5, 6, 7, 11, 12, and 13.

51. (NEW) The kit of claim 48, comprising one or more of the following primers for amplification of $\alpha 2$: comprise Sequence ID Nos. 8, 9, 10, 14, 15, and 16.

52. (NEW) The kit of claim 48, further comprising $\alpha 1$ and $\alpha 2$ integrin subunit standards.

53. (NEW) The kit of claim 48, wherein said hybridization probe comprises 15 or more consecutive nucleotides of $\alpha 1$ integrin nucleotides 1-3900 (SEQ ID NO: 1).

REMARKS

Claims 1-30 have been canceled, and new claims 31-56 have been added. A statement to this effect is reiterated on a separate page under the heading of "Marked Up Claims." New claims 31-56 better conform to the format used in U.S. practice. No new matter has been added.

A new Abstract, conforming with that appearing on the publication page of the WIPO application, has been submitted on a separate page as required.

Respectfully submitted,

MERCHANT & GOULD P.C.
P.O. Box 2903
Minneapolis, Minnesota 55402-0903
(612) 332-5300

Date:

May 23, 2001

Denise M. Kettelberger

Denise M. Kettelberger, Ph.D.

Reg. No. 33,924

DMK:KC:PSTpmc

102050-40000060

MARKED UP SPECIFICATION AND CLAIMS

In the specification:

Page 1, after the title, the following paragraph was inserted:

--This application is a Nonprovisional of U.S. Provisional Application No. 60/001,387 filed on July 21, 1995; U.S. Provisional Application No. 60/001,861 filed on August 3, 1995; and U.S. Provisional Application No. 60/016,700 filed May 2, 1996.--

In the claims:

Claims 1-30 have been cancelled.

Claims 31-56 have been added.

ABSTRACT

Analysis of alterations in integrin subunit expression, particularly $\alpha 1$ and/or $\alpha 2$ integrin subunit expression from integrin producing cells as compared to normal controls as a diagnostic method to identify individuals who have or are predisposed to pathologies associated with altered matrix deposition, such as diabetic renal nephropathy.

102050-400000



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Tsilibary, Photini-Effie, et al.

Serial No: PCT/USUnknown (based on
PCT/US96/12067)

Int'l Filing Date: Concurrently Herewith

Docket No.: 600.314USWO

Due Date: January 21, 1998

Title: ANALYSIS OF ALPHA INTEGRINS FOR THE DIAGNOSIS OF DIABETIC NEPHROPATHY

CERTIFICATE UNDER 37 CFR 1.10:

"Express Mail" mailing label number: EM045419937US

Date of Deposit: January 21, 1998

I hereby certify that this paper or fee is being deposited with the United States Postal Service "Express Mail Post Office to Addressee" service under 37 CFR 1.10 on the date indicated above and is addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231.

By: 

Name: William Smith

Assistant Commissioner for Patents

Attn: BOX PCT

Washington, D.C. 20231

Sir:

We are transmitting herewith the attached:

- ☒ Transmittal sheet in duplicate containing Certificate under 37 CFR 1.10.
- ☒ A check in the amount of \$ 1372.00 to cover filing fee.
- ☒ A return postcard.
- ☒ Other: PTO-1390 (2 pages)

Please charge any additional required fees or credit overpayment to Deposit Account No. 13-2725 A
duplicate copy of this sheet is enclosed.

MERCHANT, GOULD, SMITH, EDELL, WELTER & SCHMIDT
3100 Norwest Center, Minneapolis, MN 55402 (612/332-5300)

By: 

Name: Steven C. Bruess

Reg. No.: 34,130

Initials: SCB/IPD/KMC/mls

09/000004

10 Rec'd PCT/PTO 21 JAN 1998

ANALYSIS OF ALPHA INTEGRINS FOR THE
DIAGNOSIS OF DIABETIC NEPHROPATHY

Background of the Invention

5 Diabetic nephropathy is a major cause of renal failure in the U.S. and develops in approximately 30% of insulin dependent diabetes mellitus (IDDM) patients. Recent studies by the Diabetes Control and Complications Trial Group have indicated that intensive insulin treatment substantially reduces the risk of developing complications, including nephropathy. However, the cost and effort of the intensive therapy, as well as
10 the danger of hypoglycemic attacks dictate that this treatment should be limited to those patients who are prone to develop complications. It follows that an early selection of these diabetic subjects would be extremely helpful, but currently there are no adequate predictors available for clinical use.

Metabolic imbalance caused by hyperglycemia has been implicated as a major
15 factor in the development of this condition and is associated with a genetic tendency to develop nephropathy. A prominent expansion of the mesangium with changes in the composition of the mesangial matrix have been observed in diabetic nephropathy (Williamson et al., *Diabetes Met. Rev.* 4:339 (1988), Steffes, M.W., et al. *Diabetes* 38:1077-81 (1989)).

20 Studies performed with human and experimental animal mesangial cells cultured in high-glucose medium have demonstrated an increased synthesis and accumulation of matrix proteins, namely collagens, including collagen type IV and fibronectin. This suggests that hyperglycemia plays a role in the mesangial changes of diabetic nephropathy. Ayo, S.H., et al. (1990a), *Am. J. Pathol.* 136:1339-1348; Nahman, N.S.,
25 et al., *Kidney Int.* 41:396-402 (1992); Danne, T., et al., *Diabetes* 42:170-177 (1993). The changes in the matrix secretion pattern of the cell are mediated either directly by hyperglycemia or by the glycation of mesangial matrix on prolonged exposure to high levels of glucose. Studies have demonstrated that cultured mesangial cells are influenced by the glycation of matrix leading to altered cell adhesion, spreading and
30 proliferation. Since collagen IV (cIV) is the major component of the mesangial matrix (about 60%), changes in the interactions between this major mesangial glycoprotein and mesangial cells may play an important role in the pathology of diabetic nephropathy. Kim, Y., et al., *Am. J. Pathol.* 138:413-420 (1991). The changes in matrix deposition

are secondary in time to insulin insufficiency. Altered matrix deposition including basement membrane thickening is also found in a variety of arterioles and arteries in patients with diabetes mellitus. Altered matrix deposition is found in the pancreas of diabetic patients. Altered matrix deposition puts diabetic patients at risk for developing secondary pathological changes including, but not limited to nephropathy, myocardial infarction, cerebral stroke, problems associated with reduced circulation, retinopathy, neuropathies and the like.

Cell-matrix interactions are mediated, for the most part, by a family of receptors known as integrins. The very late antigen (VLA) subgroup of integrins which share a common $\beta 1$ chain, include the cell membrane receptors for αIV , $\alpha 1\beta 1$ and $\alpha 2\beta 1$. Although integrins are mainly studied for their role in cell differentiation, migration and signaling events, they may also be involved in the maintenance of tissue structure. For instance, cells can modify their matrix by altering the production of matrix proteins and/or by regulating matrix organization. Cells cultured under high glucose conditions resulted in an increased production of matrix components by mesangial cells. (Kashgarian, M., et al., *Kidney Int.* 41:524-529 (1992).) The balance of cell surface integrin expression has been demonstrated to be altered in various disease states including inflammation and malignancy (Waes and Carey, *Otolaryngologic Clinics of North America* 25(5):1117 (1992); Adams, J.C., et al., *Cell* 63:425-435 (1990); Rozzo et al., *FEBS Letters* 332:263 (1993)). This altered expression has been associated with altered adhesion to extracellular components.

Presently, the only earliest available indicator of kidney changes is microalbuminuria which occurs after the appearance of nephropathic changes. Yet only a percentage of individuals with microalbuminuria go on to develop glomerulopathy. Individuals at risk for developing glomerulopathy are best treated with intense glucose-modulating therapies that have their own risk. Often physicians are hesitant to place individuals with microalbuminuria on such therapies since the majority of these patients do not proceed to glomerulopathy. Biopsies indicating the accumulation of matrix accompanying the expansion of the mesangium occur at a point when the process has become irreversible. Therefore an early predictor of nephropathy or other disease states associated with altered matrix deposition would be beneficial as an indicator of those

patients who require stringent control of blood glucose levels to minimize nephropathic and other altered matrix deposition-associated disorders.

Thus, there is a need to identify markers associated with the changes seen in nephropathy and in other altered matrix deposition-associated disorders for the
5 diagnosis of these disorders. There is a need to identify changes in regulation and function of integrins in diabetic patients and there is a need to develop a diagnostic test that can be used to identify patients who are likely to develop or have the early symptoms of nephropathy.

10

Summary of the Invention

Alterations in the amounts and patterns of alpha-integrin subunits has now been correlated to the onset of nephropathy. Analysis of alpha integrin subunit expression as compared with controls provides a diagnostic tool for the determination of patients likely to develop severe nephropathy and a method to monitor progress of disease
15 during treatment protocols.

15

Cells that express alpha integrins, such as kidney tissue, fibroblasts, endothelial cells, and blood cells are analyzed for alpha integrin subunit expression, for example, by *in situ* hybridization methods. Changes in the amounts and pattern of integrin subunit expression as compared with control samples, is diagnostic of nephropathy and can be
20 used to screen individuals, e.g., diabetic patients at risk for developing severe disease.

20

Analysis of $\alpha 1$, $\alpha 2$, $\alpha 3$, $\alpha 5$, and beta-1 integrin subunit expression as compared with control tissue expression is preferred. An increase in $\alpha 2$, $\alpha 3$, $\alpha 5$, or beta-1 integrin expression and/or a decrease in $\alpha 1$ expression is diagnostic of increased risk of nephropathy. An especially preferred diagnostic method is the comparison of $\alpha 1$ and $\alpha 2$
25 integrin subunit expression with control tissue. A pattern change including a decrease in $\alpha 1$ and an increase in $\alpha 2$ is diagnostic of increased risk of nephropathy or onset of the disease.

25

Brief Description of the Drawings

30

Figure 1 is a histogram summarizing results of *In situ* hybridization studies of rat control and diabetic tissue with $\alpha 1$ and $\alpha 2$ integrin probes.

Detailed Description of the Invention

Analysis of changes in the pattern of integrin subunit expression, particularly of alpha integrin subunits, is made by comparing expression in sample tissues as compared with tissue controls.

5

Tissue Samples:

The invention is directed to methods of detecting changes in α integrin subunit expression in cells, such as the cell populations (visceral epithelial, endothelial and mesangial and other matrix-producing cells) present in the glomerulus; and also in the tubules as well as including, but not limited to, fibroblasts (for example see D. Kyu Jin, et al. in *J. Am. Society of Nephrology*, 5(3): 966, 1994), epithelial, and endothelial cells from a variety of tissues and organs as well as blood cells including, but not limited to polymorphonuclear leukocytes, monocytes, and the like. Changes to blood cells, including leukocytes, have been reported in diabetic patients who develop nephropathy (Ng, et al. *Diabetologia* 33:278-284, 1990).

15

A change in the expression of $\alpha 1$ and $\alpha 2$ integrins has been detected in the studies disclosed here, under conditions of high glucose (i.e., about 25 mM) compared with low glucose (i.e., about 5 mM), in diabetic test animals *in vitro*, and in a human diabetic patient with neuropathy. Mesangial cells cultured in high glucose showed an increase in $\alpha 2$ integrin expression and a decrease in $\alpha 1$ integrin expression compared with mesangial cells grown under low glucose conditions. A change in expression of α integrins such as $\alpha 1$ and/or $\alpha 2$ subunits can be used to identify patients that have or will develop diabetic nephropathy. In view of these studies, it is believed that patients showing about a 25 to 100% decrease in $\alpha 1$ integrin and/or about a 25 to 100% increase in $\alpha 2$ integrin expression have a greater chance of developing diabetic nephropathy. The methods disclosed here are useful to identify diabetic patients at risk for developing diabetic nephropathy. The methods may also be useful to monitor progression of diabetic nephropathy. Patients identified as having a risk for developing or showing early symptoms of diabetic nephropathy can be placed on a strict glucose control regimen so that the development and/or progression of nephropathy can be inhibited.

20

25

30

Changes in integrin subunit expression in diabetic patients have been identified in cultured human skin fibroblasts taken from skin biopsies (D. Kyu Jin, et al., *J. Am.*

Soc. of Nephrology 5(3):966, 1994) suggesting that a variety of integrin-expressing cells could be monitored to identify individuals with a predisposition to nephropathy or to other complications associated with diabetes-induced altered matrix deposition.

5 **Methods of Detecting a Change in Expression of α 1 and/or α 2 Integrin Subunits in Cells from Diabetic Patients**

The methods of the invention are conducted with cell types that express alpha (α) integrin subunits. Preferably, to identify patients predisposed to nephropathy, the cells are obtained from tissue samples from biopsy of kidney tissue of diabetic patients.

10 However, other cell types that express α integrin subunits can be utilized including, but not limited to, fibroblasts, endothelial cells, polymorphonuclear leukocytes, monocytes, and other blood cells. The amount of cells typically obtained is relatively small so that the detection methods selected are those that can detect and/or quantitate α integrin subunit expression in a small cell sample. These methods include, but are not limited to
15 *in situ* hybridization, including polymerase chain reaction (PCR) enhanced *in situ* hybridization (also known as *in situ* PCR) and the like.

The cell samples are obtained from patients having diabetes but having no demonstrable symptoms or signs of nephropathy. The earliest change in nephropathy is the detection of microalbuminuria. Biopsy specimens may also be obtained from
20 diabetic patients that may have early symptoms of nephropathy so that the progression of diabetic nephropathy can be monitored. Blood samples and skin biopsies also can be obtained from patients with diabetes and processed for either *in situ* hybridization or PCR enhanced *in situ* hybridization (also known as *in situ* PCR). Similarly, it is possible to perform *in situ* hybridization or PCR enhanced *in situ* hybridization using a
25 cheek scraping or a scraping of other accessible tissue.

Biopsy tissue samples are usually about 1 mm³ and are obtained using standard biopsy methods. Where the kidney is the organ selected for biopsy, kidney tissue from the cortical region is preferred although biopsy samples can be obtained elsewhere. Fibroblasts can be obtained from skin or any other tissue. The biopsy samples are then
30 frozen in liquid nitrogen or fixed in 4% fresh paraformaldehyde and sectioned into 5 μ m thick sections on silane-coated slides. The sections can then be treated with reagents to detect and/or quantitate α integrin expression in cells.

Blood cells and other α integrin expressing cells can also be analyzed for changes in α integrin subunit expression. These cells include fibroblasts, monocytes, polymorphonuclear leukocytes and other blood cells. Cells can be obtained and isolated from a blood or bone marrow sample. Methods for isolating particular cell types from a blood sample are well known in the art. Preferably leukocytes are isolated from blood by centrifugation, followed by hypotonic shock of residual blood cells as disclosed by Ng, et al. *Diabetologia* 33:278-284, 1990.

Rather than preparing cell sections, the sample of cells can be extracted to obtain nucleic acids using standard methods. The nucleic acids encoding $\alpha 1$ and/or $\alpha 2$ integrin subunits can be amplified using any of a variety of polymerase chain reaction methods. For example, changes in the level of expression of $\alpha 1$ and/or $\alpha 2$ integrins can be detected using a competitive PCR method as described by Gilland, G., *Proc. Natl. Acad. Sci. (USA)* 87:2725 (1990).

In a method of the invention, the level of $\alpha 1$ integrin expression is detected and/or quantitated in cells such as glomerular and tubular kidney cells. The level of $\alpha 1$ integrin expression can be detected using a variety of standard methods. The preferred methods are *in situ* hybridization, *in situ* PCR for detection of integrin RNA and immunofluorescence detection of antibody-tagged integrin protein. A decrease of about 25 to 100% in $\alpha 1$ integrin expression can indicate that early changes of diabetic nephropathy are occurring and can be used to identify patients that have an increased risk of developing diabetic nephropathy. A decrease in $\alpha 1$ integrin expression is compared to the level of $\alpha 1$ integrin expression in cells from age matched non-diabetic controls.

For detection and quantitation using *in situ* hybridization, the following method is preferred: a detectably labeled probe that is complementary to and/or hybridizes to all or a portion of nucleic acid sequences encoding all or a portion of $\alpha 1$ integrin subunit is utilized. A radioactively labeled probe preferably has a specific activity of about 2×10^8 to 1×10^9 dpm/ μ g. *In situ* hybridization on cells such as kidney tissue can be conducted as follows. 5 μ m tissue sections, fibroblasts and/or blood cells on silane-coated slides are further fixed in fresh 4% paraformaldehyde for 10 min. The slides are then pretreated with 0.2N HCl for 20 min., 0.05 M Triethanolamine (TEA, Sigma) for 15 min, 0.005% digitonin for 5 min., 3 μ g/ml proteinase K (Sigma) for 15 min. at 37°C,

and 0.3% acetic anhydride - 0.1M TEA for 10 min. Hybridization is performed at 50°C overnight in 50% formamide, 0.6 M NaCl, 1xDenhardt's, 0.17 µg/ml human COT^{RT} DNA (GIBCO/BRL), 1 mg/ml poly A (Boehringer Mannheim), 10% (W/V) Dextran sulfate (Sigma), 0.1 M dithiothreitol (DTT, Boehringer Mannheim), 1 mM EDTA, 0.1 mM aurintricarboxylic acid (ATA, Sigma) and S³⁵-dCTP labeled cDNA probe. The following day, the slides are washed in 2x SCC-0.05% SDS for 60 min. at 55°C; further washed in the high stringency washing buffer containing 50% formamide, 0.6 M NaCl, 1 mM EDTA, 5 mM DTT and 10 mM Hepes for 4 days at room temperature. After 4 days, the slides are rinsed in 2x SCC and the slides are dehydrated in graded ethanol with 0.3 M ammonium acetate, then dipped in Kodak NTB-2 emulsion and exposed for 5 days at 4°C. After development, the slides are stained with hematoxylin-eosin (Surgipath Canada, Inc., Winnipeg, Canada) and mounted. The silver grain number per cell are used to quantitate the result of *in situ* hybridization. About 10-20 glomeruli and a similar number of tubules are examined per patient.

A probe of the invention hybridizes to and is complementary to and/or all or a portion of a nucleic acid sequence encoding $\alpha 1$ integrin as long as the probe specifically detects $\alpha 1$ integrin expression. Probes can be designed using a known sequence such as the rat $\alpha 1$ integrin sequence as shown as Figure 2 in Takada and Hemnlev, *J. Cell Biol.* 109:397-407 (1983) or by the use of commercially available programs and are capable of binding to rodent or human $\alpha 1$ integrin but are not capable of binding to other proteins including other proteins having regions homologous to α integrins when tested under identical hybridization conditions. Examples of other proteins that have homologous regions to α integrins include those proteins identified using a gene bank search, such as GenBank, or the like, or in publications related to $\alpha 1$ and $\alpha 2$ subunits (for example, see Ignatius, et al. *J. Cell Biol.* 111:709-720, 1990 listing proteins with homologies to the $\alpha 1$ -subunit).

The probe can be about 15 nucleotides long up to a full length probe of about 4kb. The probes are preferably 100% complementary to the nucleic acid encoding $\alpha 1$ integrin however some mismatches can be present depending on the length of the probe. About 1 to 3 mismatches in a probe of about 20 to 30 nucleotides long can be present as long as hybridization conditions are adjusted to account for mismatches. Hybridization conditions can be adjusted to take into account mismatches in accord with known

principles as described in Sambrook et al., A Guide to Molecular Cloning, Cold Spring Harbor NY (1989).

A specific example of a nucleic acid sequence encoding $\alpha 1$ integrin is the rat $\alpha 1$ integrin sequence shown as Figure 2 in Ignatius et al., *J. Cell. Biol.* 111:709-720, 1990, (SEQ ID NO:1) and the protein sequence encoded by $\alpha 1$ integrin is provided as SEQ ID NO:2. A DNA sequence encoding $\alpha 1$ integrin can be obtained from a rat pheochromocytoma cell line PC12 as described by Ignatius et al., *J. Cell. Biol.* 111:709 (1990). Briefly, a cDNA library can be prepared from rat pheochromocytoma PC12 in a lambda vector. The sequence can be identified and/or amplified using probes or primers designed from the known sequences using standard methods as described in Sambrook et al., (*supra*). Once the sequence is subcloned it can be confirmed by sequence analysis and/or by screening with antibodies specific for $\alpha 1$ integrin. Other DNA sequences encoding $\alpha 1$ integrins can be identified and isolated using probes and primers derived from the known sequences.

A preferred probe is a 3.9 kb fragment from the 5' end through the EcoR1 site near base 3900 including the sequence as shown in Figure 2 of Ignatius et al. (*supra*). Smaller fragments that can form probes can readily be prepared with restriction enzymes or derived by automated or manual oligonucleotide synthesis techniques, by PCR, or by other methods also known in the art. The probes are preferably detectably labeled with a radioactive nucleotide using standard methods.

Other methods utilizing probes for detection of $\alpha 1$ integrin expression can also be utilized using standard methods such as Northern Blot Analysis and the like as described in Sambrook et al., cited *supra*.

Primers can also be designed based upon the sequence of rat $\alpha 1$ integrin sequence. This invention also contemplates using primers and nucleic acid sequences from the human $\alpha 1$ integrin sequence provided by Briesewitz, et al. (*J. Biol. Chem.* 268(4):2989-96, 1993). Primers can be designed using a known sequence using commercially available computer programs. Primers typically are complementary to and/or hybridize to a 5' region and/or a 3' region of the nucleic acid sequence encoding the protein of interest. The primers can be used to amplify all or a portion of DNA or cDNA encoding $\alpha 1$ integrin. Primers can be used to make probes and to detect expression levels of $\alpha 1$ integrin. Primers preferably have at least 15 nucleotides that are

100% complementary to the nucleotide sequence selected. The primers can also have additional sequences preferably at the ends of the primer that include restriction enzyme sites and the like that are not complementary to the nucleic acid sequence to be amplified. Primers are preferably about 15 to 50 nucleotides long and can be prepared by automated synthesis.

The primers can be used to detect the level of $\alpha 1$ expression in cells. RNA from cells is extracted and reverse transcribed using standard methods. Primers that are complementary to and can hybridize to a DNA sequence encoding $\alpha 1$ integrins are utilized to amplify the cDNA. A decrease in the level of PCR product can be determined in comparison to the amount of PCR product obtained from control cells.

One method of utilizing PCR to detect $\alpha 1$ integrin expression is *in situ* PCR. A method for PCR *in situ* hybridization is described in PCR In Situ Hybridization Protocols and Applications, J. Novo ed., "PCR *In Situ* Hybridization", pp. 157-183. Briefly, tissue sections, fibroblasts and/or blood cells (about 5 μm) are placed on silane-coated glass slides. After removing paraffin, the slides are treated with trypsinogen (2mg/ml) in 0.01N HCl for 10 minutes and then trypsinogen inactivated in 0.1M Tris HCl (pH 7.0) solution. The slides are washed sequentially in 90% and 100% ethanol, two times for 1 minute each and air dried. Aliquots of reaction mixture containing 0.15 units/ml *Taq* DNA polymerase and specific primer pairs for $\alpha 1$ integrin are added to the tissue section and then overlaid with siliconized glass coverslips. The slides are placed in the heat-sealable plastic bags and 4-5ml mineral oil is added. After removing air, the bag is heat-sealed and placed in the thermal-cycling oven for 40 cycles. After thermal-cycling, the slides are washed twice in chloroform for 2 minutes. The coverslips are removed and the slides are dipped briefly in fresh chloroform. After washing in PBS for 5 minutes, the slides are dehydrated and air-dried. The slides are dipped in NTB2 nuclear emulsion (Kodak) and exposed in the dark for 7 days. After development, the slides are *counterstained* with hematoxylin-eosin.

A change in the level of $\alpha 1$ integrin protein expression can also be detected by using immunofluorescence. (Unless otherwise specified as "protein expression", the term "expression" used herein generally refers to RNA expression.) Sections of tissue samples, fibroblasts and/or blood cells can be stained with antibodies specific for $\alpha 1$ integrin. It is preferable that antibodies are monoclonal antibodies and are antibodies

that do not substantially cross-react with other α integrin subunits. Antibodies to $\alpha 1$ integrin can be made by standard methods such as described in Wayner EA and WG Carter, 1987, *J. Cell Biol.* 121(5):1141-1152. Antibodies specific to $\alpha 1$ integrin include the SR84 and TS2/7 antibodies. Information related to these antibodies is provided in

5 Examples 1 and 3. A decrease in the level of immunofluorescence can be observed and quantitated using standard methods. A decrease of about 25 to 100% of $\alpha 1$ integrin expression may be used to identify patients that have a greater risk of developing diabetic nephropathy. A decrease in $\alpha 1$ integrin expression is compared to the level of $\alpha 1$ integrin expression in age-matched nondiabetic controls.

10 The preferred method of the invention involves comparing the level of expression of $\alpha 2$ integrin to the level of expression of $\alpha 1$ integrin. Under high glucose conditions, a decrease in the level of $\alpha 1$ expression is seen as well as an increase in the level of $\alpha 2$ expression in mesangial cells. It is believed that patients at greater risk for nephropathy or other complications associated with diabetes will exhibit an increase in

15 $\alpha 2$ expression and a decrease in $\alpha 1$ expression. A change of about 15 to 100%, and preferably of about 25 to 100%, of $\alpha 2$ integrin expression as well as a change of about 15 to 100%, and preferably of about 25 to 100%, of $\alpha 1$ integrin expression is believed to be indicative of patients with a greater risk of developing diabetic nephropathy.

Integrin expression is associated with a variety of cell types in a variety of

20 locations throughout the body, therefore it is possible that altered levels of integrin expression will also be identified in diabetic associated retinopathy, atherosclerosis and select diabetic neuropathies.

The expression of integrin subunits, preferably of $\alpha 1$ and $\alpha 2$ integrin subunits, is detected and/or quantitated in tissue samples, fibroblasts and/or blood cells from

25 diabetic patients. The preferred methods are those that allow detection of gene expression in a small amount of cells or tissue.

The expression of $\alpha 2$ integrin can be detected using *in situ* hybridization. The conditions for *in situ* hybridization are the same as those described previously. A probe specific for nucleic acid sequences encoding $\alpha 2$ integrin can be prepared using standard

30 methods as described in Sambrook et al., cited *supra*. The probes are complementary to and/or hybridize to all or a portion of a nucleic acid sequence encoding $\alpha 2$ integrin. As described for $\alpha 1$ integrin, the probe to detect $\alpha 2$ integrin can hybridize to a portion of a

nucleic acid sequence as long as the probe specifically detects a sequence encoding $\alpha 2$ integrin. Nucleic acid sequences can be DNA, cDNA, or RNA. It is preferred that the probe hybridize to RNA or cDNA.

A specific example of nucleic acid sequence encoding $\alpha 2$ integrin is shown in
5 Figure 2 of Takada and Hemler, *J. Cell Biol.* 109:397 (1989). (SEQ ID NO:3). DNA
sequence encoding human $\alpha 2$ integrin can be isolated as described in this reference.
The protein encoded by SEQ ID NO:3 is provided in this disclosure as SEQ ID NO:4.
Nucleic acid sequences encoding $\alpha 2$ integrin can be obtained from human lung
fibroblasts and/or human endothelial cells. Preferably DNA libraries from endothelial
10 cells can be prepared and nucleic acids encoding $\alpha 2$ integrin identified and/or amplified
using probes and primers derived from the sequence of $\alpha 2$ integrin, e.g., as shown in
Figure 2 of Takada et al. (*supra*). If primers are selected, DNA sequences can be
amplified using the polymerase chain reaction and then subcloned. Clones that are
positive by hybridization to a probe specific for DNA sequences encoding $\alpha 2$ integrin
15 (see Examples 1 and 3) or that express proteins that are positive by reacting with an
antibody specific to $\alpha 2$ integrin such as P1H5 are selected. A DNA sequence encoding
 $\alpha 2$ integrin can be confirmed by DNA sequencing in comparison to the known $\alpha 2$
sequence, as shown in Figure 2 of Takada et al. (*supra*).

A probe of the invention hybridizes to and is complementary to and/or
20 hybridizes to all or a portion of a nucleic acid sequence encoding $\alpha 2$ integrin as long as
the probe specifically detects $\alpha 2$ integrin expression. Probes can be designed using a
known sequence such as shown in Figure 2 of Takada et al. (*supra*) by the use of
commercially available programs.

The probe can be about 15 nucleotides long up to a full length probe of about
25 5Kb. The probes are preferably 100% complementary to the nucleic acid encoding $\alpha 2$
integrin however some mismatches can be present depending on the length of the probe.
About 1 to 3 mismatches in a probe of about 20 to 30 nucleotides long can be present as
long as hybridization conditions are adjusted to account for mismatches. Hybridization
conditions can be adjusted to take into account mismatches in accord with known
30 principles are described in Sambrook et al., A Guide to Molecular Cloning, Cold Spring
Harbor NY (1989).

A preferred probe is a 1.8 fragment kb from the 5' end through the EcoR1 site near base 1800 of the sequence shown in Figure 2 of Takada et al. (*supra*). Other probes can be derived from this fragment or from the full length sequence by use of restriction enzyme digestion. Probes can also be prepared by automated synthesis or by PCR. Probes are preferably detectably labeled with a radioactive nucleotide using standard methods.

Probes specific for $\alpha 2$ integrin expression can then be utilized in methods of detecting $\alpha 2$ integrin expression in various cell types. The preferred method is by use of *in situ* hybridization or PCR-*in situ* hybridization on kidney as well as other tissues. The method utilized for *in situ* hybridization has been described previously (Takada and Hemler, *supra*). The method for PCR *in situ* hybridization has been described for $\alpha 1$ integrin. Other methods utilizing probes for detection of $\alpha 2$ integrin expression can also be utilized using standard methods such as Northern Blot Analysis, and the like, as described in Sambrook et al. cited *supra*.

Primers can also be designed based upon the known DNA sequence encoding human $\alpha 2$ integrin. Primers can be designed from a known sequence such as shown in Figure 2 of Takada et al. (*supra*), using commercially available software. Primers typically are complementary to and/or hybridize to a 5' region and/or a 3' region. The primers can be used to amplify all or a portion of DNA or cDNA encoding $\alpha 2$ integrin. Primers can be used to make probes and to detect expression levels of $\alpha 2$ integrin. Primers preferably have at least 15 nucleotides that are 100% complementary to the nucleotide sequence selected. The primers can also have additional sequence preferably at the ends of the primer that include restriction enzyme recognition sites and the like. Primers are preferably about 15 to 50 nucleotides long and can be prepared by automated synthesis.

Primers can be used to detect the level of $\alpha 2$ integrin expression in cells. Nucleic acids, preferably RNA, from cells from diabetic patients are extracted and reverse transcribed using a standard method. Primers that are complementary to and can hybridize to a cDNA sequence encoding $\alpha 2$ integrin are utilized to amplify the cDNA. An increase in the level of PCR product can be determined in comparison to the amount of PCR product obtained from control cells.

A change in the level of $\alpha 2$ integrin protein expression can also be detected by using immunofluorescence. Sections from kidneys and/or other tissues, skin fibroblasts and/or blood cells can be incubated with antibodies specific to $\alpha 2$ integrin. It is preferable that the antibodies are monoclonal antibodies and are antibodies that do not crossreact with other α integrin subunits. Antibodies to $\alpha 2$ integrin can be made by standard methods such as described in Wayner EA and WG Carter, 1987, *J. Cell Biol.* 121(5):1141-1152. Antibodies specific for $\alpha 2$ integrin include P1H5. An increase in the level of immunofluorescence can be observed and quantitated using standard methods such as flow cytometry. An increase of about 25 to 100% of $\alpha 2$ integrin expression can be used to identify patients that have a greater risk of developing diabetic nephropathy. An increase in $\alpha 2$ integrin expression is compared to $\alpha 2$ integrin expression in nondiabetic control cells.

An increase in $\alpha 2$ integrin expression alone can also be used to identify a patient that may have a greater risk of developing diabetic nephropathy. An increase in $\alpha 2$ expression can be determined as described using the methods described above. An increase of about 25 to 100% in $\alpha 2$ integrin expression may indicate a patient who has an increased risk of developing diabetic nephropathy.

Although an increase of $\alpha 2$ integrin expression or a decrease of $\alpha 1$ integrin expression alone can be utilized to identify patients at greater risk for developing diabetic nephropathy, a preferred method is to detect changes in both $\alpha 1$ and $\alpha 2$ integrin expression. It is believed that an increase in $\alpha 2$ integrin expression and a decrease in $\alpha 1$ integrin expression identifies patients that are at greater risk of or are showing early symptoms of diabetic nephropathy.

In one step of the method, the level of $\alpha 2$ to $\alpha 1$ integrin is compared. The level of $\alpha 1$ integrin expression can be detected and/or quantitated using the methods described previously. The level of $\alpha 1$ and $\alpha 2$ integrin expression can be quantitated on two different cell samples such as two sections of the same tissue sample. About 10-20 glomeruli and tubules are examined. On one cell sample containing the same type of cells, $\alpha 2$ integrin expression can be quantitated and on a second cell sample with the same type of cells, $\alpha 1$ integrin expression can be quantitated. Alternatively, the level of $\alpha 1$ and/or $\alpha 2$ integrin expression can be determined using the same cell sample if the agent used to detect $\alpha 1$ expression is detectably labeled with a first detectable label and

the agent used to detect $\alpha 2$ expression is detectably labeled with a second detectable label. The first detectably labeled agent and the second detectably labeled agent are agents selected that can be detected and/or quantitated in the presence of one another.

In a preferred version, kidney tissue sections taken from diabetic patients are
5 fixed in formalin and then treated with HCl and proteinase K. A first probe specific for $\alpha 1$ integrin is a 3.9 kb fragment from 5' end through EcoR1 site near base 3900 probe including a sequence as shown in Figure 2 of Ignatius et al. (*supra*). This probe is labeled with ^{32}P or ^{35}S or other suitable labels known in the art including, but not limited to, fluorescent labels, biotinylated labels, or other radio labels and the like. The
10 probe is incubated with the section as described previously. A second section taken from the same tissue sample is treated in the same manner but incubated with a probe specific for $\alpha 2$ integrin expression. In a preferred embodiment, a probe specific for $\alpha 2$ integrin expression is a 1.8 kb fragment from 5' end through EcoR1 site near base 1800 that includes a sequence as shown in Figure 2 of Takada et al. (*supra*). Both probes are
15 labeled with ^{32}P or ^{35}S . The probe is incubated with the section overnight at 50°C and then for 4 days at room temperature. The sections are then developed for autoradiography. The number of grains per cell are counted for about 10-20 glomeruli and tubules. The total counts for $\alpha 2$ integrin expression vs. $\alpha 1$ integrin expression are compared. An increase of about 40% in $\alpha 2$ integrin and a 30-40% decrease of $\alpha 1$
20 integrin may indicate a patient is at greater risk for developing diabetic nephropathy.

In an alternative version, the level of expression of $\alpha 2$ integrin is compared with the $\alpha 1$ expression which can be determined using *in situ* PCR or competitive reverse transcriptase PCR. Primers specific for $\alpha 1$ and $\alpha 2$ integrin expression can be prepared as described previously. For competitive reverse transcriptase PCR, RNA extracted
25 from different cell types obtained from diabetic patients will be reverse transcribed to generate cDNA. The cDNA will be mixed with the various concentrations of competitive template amplified by the PCR method. After degradation of competitive cDNA with restriction enzyme, amplified cDNA will be subjected to electrophoresis in 2% agarose gel, electrotransferred to a nylon membrane, UV cross-linked to the
30 membrane and hybridized with a ^{32}P -labeled probe. Autoradiographs will be used to quantify the label bound to the cDNA using amount of label bound to samples containing target cDNA alone as compared to samples also containing competitor

cDNA to arrive at the target cDNA concentration. For *in situ* PCR, a method has been described previously. The change in $\alpha 1$ and $\alpha 2$ integrin expression can be quantitated by counting the number of grains per cell in control vs. diabetic cells.

Optionally, for each of the detection methods for α integrin subunits, the level of integrin subunit expression can be compared to expression of a control. The control is selected to be a protein expressed at the same levels in both normal and diabetic cells. The control protein is also selected to be one that is expressed at sufficient levels for easy detection and quantitation. The level of expression of $\alpha 1$ and $\alpha 2$ integrin expression can each be compared to that of the level of the control RNA expression in the cells. The level of RNA expression of $\alpha 1$ integrin or $\alpha 2$ integrin can be divided by the level of expression of the control RNA to normalize the values to the level of control expression in a particular cell sample. The level of expression of the control protein is detected and quantitated using the same method as $\alpha 1$ or $\alpha 2$ integrin expression. The preferred control protein is a cell surface HLA determinant.

Optionally, the levels of $\alpha 3$, $\alpha 5$, or beta-1 integrin subunit expression can be analyzed as described above. The level of $\alpha 3$, $\alpha 5$, or beta-1 integrin expression in cells such as kidney tissue can be detected and quantitated as described for $\alpha 1$ and $\alpha 2$ integrin expression including *in situ* hybridization, *in situ* PCR, immunofluorescence and the like. Other cell types can be analyzed as described above, including fibroblasts and blood cells. Antibodies specific for $\alpha 3$, $\alpha 5$, and beta-1 can be prepared as described by Wayner et al. cited *supra*.

A DNA sequence encoding $\alpha 3$ integrin has been described in Takada et al., *J. Cell Biol.* 115:257 (1991). A probe specific for cDNA sequence encoding $\alpha 3$ integrin subunit is a 1.4Kb Sal I fragment containing 5' untranslated and amino terminal coding sequences for $\alpha 3$ subunit of integrin. DNA sequences encoding $\alpha 3$, $\alpha 5$, and beta-1 integrin can be utilized to form primers and probes as described previously.

The level of $\alpha 3$, $\alpha 5$, or beta-1 integrin expression is increased about 15 to 100% compared with cells from age matched nondiabetic controls. It is believed that an increase in $\alpha 3$, $\alpha 5$, or beta-1 integrin subunit expression may also identify patients that have an increased risk of developing diabetic nephropathy or that have early signs of diabetic nephropathy.

This invention also relates to methods for detecting alterations in integrin subunit expression, particularly $\alpha 1$ and/or $\alpha 2$ integrin subunit expression by obtaining a cell sample from a patient, processing the sample to detect alterations in integrin subunit expression as compared to integrin expression in samples from age matched normal controls, detecting levels of integrin expression and determining if these levels are altered relative to controls.

This method is useful for predicting individuals at risk for developing pathologies associated with altered cell matrix deposition, including but not limited to renal nephropathy. In preferred embodiments of this invention, the tissues used to detect altered $\alpha 1$ and/or $\alpha 2$ integrin expression include kidney biopsies, skin biopsies and blood cells including polymorphonuclear cells, monocytes, and other cells expression integrin subunits. Biopsied tissue can be further separated into its cellular components or processed as tissue sections for *in situ* hybridization techniques, and/or for immunodiagnostic techniques including immunofluorescence and immunoperoxidase staining.

The cellular components of the biopsied tissue can be cultured for *in vitro* studies including Northern procedures, PCR techniques, immunofluorescent techniques and/or *in situ* hybridization techniques. Alternatively, cells can be separated and analyzed by flow cytometry, immunofluorescence, processed for PCR or for any of a variety of techniques discussed throughout this disclosure.

While blood cell components are preferably separated from the whole blood sample using methods well known in the art. Individual cells are separated, where necessary, using techniques such as those of Ng, et al. (*supra*), and Baron, et al. *Clin. Sci.* 37:205-219, 1990. Preferably the samples are tested using *in situ* hybridization methods. Where the amount of tissue available is fairly small, PCR-enhanced *in situ* hybridization can be used.

The present invention is also directed to a kit to detect alterations in integrin subunit expression, particularly $\alpha 1$ integrin and/or $\alpha 2$ integrin subunit expression in a patient sample. A variety of kits are contemplated to encompass a variety of methods. These kits optionally include reagents to process a tissue or cell sample for the technique employed by that particular kit. By example, a kit for PCR or PCR enhanced *in situ* hybridization can include reagents to process the cell sample or section and

isolate the RNA (for PCR). It will also contain suitable primers to amplify the target sequence and additional probes, if necessary, to detect the desired nucleic acid fragments as well as buffers and reagents for the polymerase chain reaction and the buffers and emulsions required to develop the silver granules, and the like, for *in situ* hybridization methods. Other kits can alternatively include reagents for immunofluorescence using antibodies to the integrin subunits and/or probes, primers and reagents for modifications of *in situ* or PCR *in situ* hybridization methods.

All publications and patent applications in this specification are indicative of the level of ordinary skill in the art to which this invention pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated by reference.

It will be apparent to one of ordinary skill in the art that many changes and modifications can be made in the invention without departing from the spirit or scope of the appended claims.

Example 1
Effect of High Glucose on the Synthesis and
Cell Surface Expression of Integrin Receptors
by Cultured Mesangial Cells

Cell lines and culture conditions

Human mesangial cells (HMC) were isolated from 19-22 week old fetal kidney tissue or adult tissue as previously described (Striker and Striker, *J. Lab. Invest.* 53(2):122-131, 1985). Cells were cultured at 37°C in an environment of 95% air and 5% CO₂ and in media composed of MEM (Sigma, St. Louis, MO) containing 5 or 25 mM glucose, 20% FBS, 15mM Hepes, penicillin (100 U/ml), streptomycin (100mg/ml), and amphotericin (25mg/ml). Cells were cultured in the two different conditions for at least two passages before they were used for experiments. Cells were released from their tissue culture flasks for passaging or for use in experiments, by washing twice with 1 mM EDTA in HBSS and then treating with 0.05% trypsin and 1 mM EDTA in HBSS for 1 min. Cells between passage 4 and 9 were used in experiments.

The cells were grown in T-75 flasks until 75-80% confluent. For the adhesion and immunoprecipitation analyses, cells were metabolically labeled for 18 hours with 0.5 mCi of [³⁵S]-methionine per T-75 flask. [³⁵S]-methionine was obtained from Du Pont/NEN, Boston, MA.

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Monoclonal antibodies (Mabs) to integrin receptors

Mabs to the integrin receptors $\alpha 3$ (P3D11), $\alpha 5$ (P3D10) and $\beta 1$ (P5D2) can be produced as previously described (Wayner et al., *J. Cell. Biol* 121(5):1141 (1993)) and are available from EA Wayner, Fred Hutchinson Cancer Center, Seattle, WA. The antibodies were characterized by sequential immunoprecipitation with known Mabs directed against these integrin receptors (P1B5, P1D6, P4C10) available from EA Wayner. Other Mabs $\alpha 2$ (P1H5), $\alpha 4$ (P4G9) and $\beta 2$ (P4H9) were previously described (Wayner et al., cited *supra* 1993) and are available from EA Wayner, Fred Hutchinson Cancer Center, Seattle, WA. TS2/7 was provided by Dr. Martin Hemler (Dana Farber Cancer Institute, Boston, MA).

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SR84 supernatant was used as a function-blocking anti- $\alpha 1$ Mab in inhibition experiments. SR84 is available from Dr. D.O. Clegg (Univ. of California, Santa Barbara, CA). ($\alpha 6$) G0H3 was purchased from AMAC Inc., Westbrook, ME. In addition monoclonal antibodies to $\alpha 1$ and $\alpha 2$ integrin were obtained from Telios Pharmaceuticals (San Diego, CA). Hybridoma culture supernatant or ascites fluid were used for immunoprecipitation, flow cytometry and inhibition experiments. A Mab directed to a cell surface HLA determinant was used as a negative control (W6/32, HB95: American Type Culture Collection, Rockville, Maryland, USA). W6/32 bound to the surface of cultured mesangial cells but did not influence adhesion of cIV. SP2 myeloma culture supernatant was also used as a control.

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Immunoprecipitation analysis of integrins from mesangial cell membranes

Mesangial cells metabolically labeled with [³⁵S]-methionine were detached from flasks by treatment with trypsin (Sigma) for 2 minutes, washed three times with phosphate-buffered saline (pH 7.4) and resuspended in PBS containing protease inhibitors (1 mM PMSF and 1 mM NEM). The radiolabeled cell membrane proteins were solubilized by adding lysis buffer (1% Triton X-100, 1 mM Calcium, 1 mM

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PMSF, 1 mM NEM and PBS at pH 7.4) and incubating for 60 minutes at 4°C. Insoluble material was separated by centrifugation at 10,000 rpm for 30 minutes.

The supernatant was transferred and 10 µl was tested for radioactivity ($\geq 10^7$ cpm/per antibody being assayed was considered to be adequate for immunoprecipitation). The lysate was precleared once with fetuin-agarose which was removed by centrifugation at 10,000 rpm for 15 minutes. This was followed by three preclears with protein A agarose bound to rabbit anti-mouse IgG, the last preclear was done overnight.

For immunoprecipitation, the cell lysate (equal counts of lysate for cells in 5 and 25 mM glucose were used) was incubated with the monoclonal antibodies to be tested, pre-bound to rabbit anti-mouse protein A-agarose. Myeloma culture supernatant was used as a negative control. Anti-HLA antibody (W6/32) was used as a control for loading. After an overnight incubation at 4°C, the agarose beads were washed five times and bound material was eluted by boiling for 5 minutes in SDS.

The eluted material was analyzed by loading lysate from each permutation on a 7.5% non-reducing SDS-PAGE gel and labeled proteins were visualized by autoradiography. The fluorograms were scanned with a Macintosh Quadra 840 computer using the NIH Image 5.1 Program, and the optical density of the bands was red after subtracting the background. The O.D. was corrected using the lanes immunoprecipitated with W6/32. Immunoprecipitation assays were performed three times for each growth condition of mesangial cells.

Immunoprecipitates were obtained with anti-integrin monoclonal antibodies from detergent extracts of metabolically labeled human kidney mesangial cells grown in 5 (low) or 25 mM (high) glucose. Equal counts of membrane proteins were immunoprecipitated to compare the level of integrin receptors of mesangial cells under the two growth conditions of low or high glucose levels.

Cells grown in 25 mM glucose have a higher specific activity of labeling than cells in 5 mM glucose. To overcome this difference and permit a comparison of the band intensity on immunoprecipitation equal counts of cell lysate from the two populations were immunoprecipitated with the antibody. Densitometry and statistical analysis of three experiments was performed, the data normalized to the HLA control and expressed as an O.D. ratio of cells grown in high glucose (HG) to cells grown in

low glucose (LG), for three experiments, with (LG = 1). Cells were labeled with [³⁵S]-methionine, the cells were harvested, and solubilized. Samples were incubated with antibody and equal counts of cell lysate from the two cell populations were immunoprecipitated with equal amounts of antibody.

5 The control indicated that there were comparable amounts of cell surface HLA determinant precipitated from each sample. W6/32, a Mab to cell surface HLA determinant was used as a negative control. Other antibodies used included an anti- α 1 antibody (TS2/7) and an anti- α 2 antibody (P1H5). In total 5 mM and 25 mM glucose exposed cell extracts were immunoprecipitated side by side 3 times.

10 The α 1 subunit band was clearly discernible at 180 kD in cell samples exposed to 5 mM of glucose and was associated with a β 1 band (116 kD). No α 1 band could be seen in the 25 mM treated cell sample. In contrast, the α 2 subunit band was more prominent in cell samples exposed to 25 mM glucose and appeared as a band at 130 kD.

15 The 130 kD α 2 band was present in 5 mM glucose but was significantly less intense than the 25 mM glucose treated samples.

 The cell lysates were also incubated with the following antibodies including: SP2 myeloma culture supernatant; anti- β 1 (P5D2), anti- β 2 (P4H9), anti- α 2 (P1H5), anti- α 3 (P3D11), anti- α 4 (P4G9), anti- α 5 (P3D10) and anti- α 6 (G0H3). Results were interpreted from three independent experiments. Immunoprecipitation of α 3- α 6 and β 1
20 integrin subunits was performed on cells from the two growth conditions. Subunits α 4 and α 6 were not detected in either cell population. The antibody to the β 1 subunit precipitated a 116 kD protein, the β 1 subunit, and also a precursor β 1 band at 105 kD. The α 3 and α 5 subunits were seen at \approx 130 kD with the associated β subunit at 116 kD, in both cell populations.

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Flow cytometry

 Cell surface expression of integrin subunits by cultured human mesangial cells was evaluated by indirect immunofluorescence staining and flow cytometry. Mesangial cells were released with trypsin, washed and resuspended in FACS buffer (HBSS, 2%
30 goat serum, 0.02% sodium azide). An equal number of cells, 2×10^5 were added to each vial.

The cells were incubated with primary antibody for one hour at 4°C and washed once with 1 ml FACS buffer. The secondary antibody was then added in a total volume of 0.5 ml FACS buffer and incubated for 30 minutes at 4°C. The cells were again washed in 1 ml of FACS buffer and resuspended in 0.5 ml of 2% formaldehyde.

5 The data was analyzed using CONSORT 30 software on a FACScan (Becton Dickinson, Mountain View, CA). Positive fluorescence was determined on a four decade log scale and fluorescence (log F1) was expressed as the mean channel number of 5,000 cells. Cell surface expression experiments were performed in duplicate with each antibody, at least three times with each growth condition of mesangial cells.

10 Densitometric scanning of the fluorograms generated from metabolically labeled cells indicated that the synthesis of the $\beta 1$ (12%), $\alpha 3$ (14%) and $\alpha 5$ (19%) were moderately increased upon growth in 25 mM glucose. Growth in 25 mM glucose dramatically decreased synthesis of the $\alpha 1$ subunit (39% reduction in intensity) while synthesis of $\alpha 2$ was considerably increased (42%).

15 These changes in metabolic activity were paralleled by a similar change in the cell surface integrin phenotype of mesangial cells grown in high glucose. To assess the effect of different glucose concentrations in the medium on the levels of mesangial cell surface integrin receptor expression cells in each glucose treatment population were stained for immunofluorescence and processed for flow cytometry. Mean channel
20 fluorescence (MCN) values of integrin subunit expression were obtained from 3 experiments. Within each experiment the ratio of MCN for cells grown in high glucose (HG) to cells grown in low glucose (LG), denominator = 1 was calculated.

 Cell surface expression of the following integrin subunits was increased by growth in high glucose: $\beta 1$ (24%), $\alpha 2$ (26%), $\alpha 3$ (18%), and $\alpha 5$ (19%). The decrease
25 in the synthesis of $\alpha 1$ was reflected in a concomitant decrease in cell surface expression (33% reduction in specific staining). The $\alpha 4$ and $\alpha 6$ subunits were not detectable in cultured mesangial cells either by immunoprecipitation or flow cytometric analyses.

 Mesangial cells grown in high glucose (for at least 2 passages) were returned to control media (5 mM glucose), again for at least 2 passages. A flow cytometric analysis
30 of these cells revealed a reversion to "low glucose" type. The expression of $\alpha 2$, $\alpha 3$, $\alpha 5$ and $\beta 1$ were decreased while the expression of $\alpha 1$ increased (data not shown).

Example 2
Adhesion of Cultured Mesangial Cells to
Type IV Collagen (cIV): Effect of High Glucose

5 Cell adhesion to collagen IV (cIV)

 The cells were detached from culture flasks by incubation with trypsin 0.05% and EDTA 0.02% for two minutes at 37°C, then washed twice with DMEM and resuspended to the appropriate concentration in binding buffer (DMEM, 25 mM HEPES, 2 mg/ml BSA at pH 7.4). 48 or 96 well plates were coated overnight at 29°C
10 with cIV in serial dilutions starting from 100 µg/ml (5 µg/96 well or 20 µg/48 well). Under these conditions approximately 50% of the cIV adhered. To block the remaining reactive sites the plates were treated with 200 µl of BSA at 2 mg/ml for 2 hours at 37°C. 50 µl of suspension containing 5000 cells (96 well plates) or 100,000 cells (48 well
15 plates) was added per well. The plates were incubated at 37°C in a humidified incubator for approximately 30 minutes. The non-adherent cells were removed by washing three times with binding buffer and then 100 µl of "lysis" buffer (0.5 NaOH, 1% SDS in distilled water) was added to each well for 30 minutes at 60°C. The lysate was
20 transferred to scintillation vials and counted. The data was expressed as a percentage of the total input cpm. Cell adhesion assays were performed in triplicate, at least three times for each growth condition.

 Cells grown in medium containing 25 mM glucose adhered significantly better than cells in 5 mM glucose. Adhesion increased with coating concentration of cIV and was saturated at 25 µg/ml for both cell populations.

25 Inhibition of cell adhesion with monoclonal antibodies

 Since growth in high glucose appeared to alter the synthesis and expression of the integrin receptors $\alpha 1\beta 1$ and $\alpha 2\beta 1$ which have been reported to be involved in cell adhesion to collagen, (Wayner and Carter, *J. Cell. Biol.* 105:1873 (1987)), we examined the effects of glucose on the ability of mesangial cells to adhere to cIV.

30 Monoclonal antibody inhibition of ^{35}S -methionine labeled human mesangial cells grown in 5 mM glucose to cIV was assessed. Briefly, 96 or 48 well plates were coated with 50 or 200 µl of cIV at 2.5 µg/ml, overnight at 29°C. The plates were incubated with 2% BSA in PBS to coat remaining reactive sites on plastic for 2 hours,

and then hybridoma culture supernatant or ascites containing 10 µg/ml of antibody were added to each well, followed immediately by the cells. After 30 minutes non-adherent cells were washed off and adherent cells were quantitated. Results were obtained from 3 experiments. SP2 myeloma culture supernatant of W6/32 were used as negative
5 controls. A quantitative ELISA was used to determine the concentration of antibody in the hybridoma culture supernatant or ascites.

In each case, the concentration of monoclonal antibody (Mab) was determined relative to a standard curve generated with an isotype-matched control mouse IgG. The concentration of antibody required to saturate the binding sites on human mesangial
10 cells was determined by flow cytometry. The concentration of the antibodies used in the inhibition assays were well above the saturating concentration as determined by flow cytometry. Data were expressed as the percent of maximal binding observed in the presence of W6/32 antibody. Inhibition experiments were performed at least three times, in triplicate, for each growth condition with the various antibodies.

15 Mesangial cells grown in high glucose (25 mM) adhered better to cIV than cells grown in low glucose (5 mM). Results indicated that adhesion increased with coating concentration of collagen IV and saturated at about 25 µg/ml for both cell populations.

In order to examine the activity of collagen receptors expressed by mesangial cells grown in high glucose, we performed adhesion experiments in the presence of well
20 characterized neutralizing antibodies directed to various β 1 integrin subunits. A panel of antibodies was used all of which have been reported to inhibit the adhesion of cells to various substrates (Wayner and Carter, cited *supra*, 1987; Wayner et al., cited *supra*, 1993). Antibodies were used at saturating concentrations as determined by immunofluorescence staining and flow cytometry. In the competition experiments, the
25 following criteria were selected to promote half-maximal binding of mesangial cells: 2.5 µg/ml cIV and a short term assay (less than 30 min). The ability of neutralizing Mabs to inhibit mesangial cell adhesion to cIV was examined in low (5 mM) or high glucose (25 mM) containing media.

To test Mab-mediated adhesion inhibition of mesangial cells grown in 5 mM
30 glucose or 25 mM glucose to collagen IV, 35 S-methionine labeled human mesangial cells were seeded in 48 well plates (100,000 cells/well) coated with 200 µl cIV (2.5 µg/ml, overnight at 29°C). Mab's anti- α 1, SR84, anti- α 2, P1H5, anti- β 1, P5D2 and

SR84 and P1H5 together, were added to the wells before seeding with cells. Adhesion in the presence of W6/32 was used as a control. After 20 minutes non-adherent cells were washed out and adherent cells quantitated. The data was expressed as a percentage of the binding in the presence of W6/32. and the two cell populations were normalized by using the binding in the presence of HLA antibody to represent 100% and the inhibition by other antibodies was calculated as a percentage of binding in the presence of HLA.

The results indicated that the $\alpha 1\beta 1$ integrin receptor had a reduced role (* $p < 0.001$) for cells grown in 5 mM glucose as compared with 25 mM glucose. Of the antibodies examined, only Mabs directed to the $\alpha 1$ (SR84), $\alpha 2$ (P1H5) or $\beta 1$ (P5D2) integrin subunits inhibited the binding of mesangial cells to cIV. When mesangial cells were grown in either low or high glucose, adhesion to cIV could be almost completely inhibited with Mabs to $\beta 1$ (P5D2) or a combination of $\alpha 1$ (SR84) and $\alpha 2$ (P1H5).

The relative effects of the neutralizing Mabs directed against the $\alpha 1$ and $\alpha 2$ subunits varied depending on whether mesangial cells were grown in low or high glucose. In 5 mM glucose the Mab to the $\alpha 1$ subunit of integrins resulted in more inhibition ($\approx 50\%$) than in 25 mM glucose ($\approx 20\%$) ($p < 0.001$). This is consistent with the presence of significantly more $\alpha 1$ integrin on the surface of cells grown in 5 mM glucose. Alternatively, in 5 mM glucose the Mab to the $\alpha 2$ subunit resulted in less inhibition ($\approx 60\%$) than in 25 mM glucose ($\approx 75\%$) ($p < 0.001$). Mab's against the $\alpha 3$, $\alpha 4$, $\alpha 5$ and $\alpha 6$ subunits did not inhibit adhesion (data not shown).

These data demonstrate that under low glucose growth conditions, mesangial cells use $\alpha 1\beta 1$ and $\alpha 2\beta 1$ integrins to bind cIV coated surfaces. However, cells grown in high glucose, appear to rely more on the $\alpha 2$ subunit complexed with $\beta 1$. The results of these functional studies are consistent with the observed alterations in the integrin cell surface phenotype discussed in Example 1.

Example 3

Localization of $\alpha 1\beta 1$ and $\alpha 2\beta 1$ Integrin Receptors

Localization of $\alpha 1$ integrin in focal adhesions

Glass cover slips were coated with 50 μ l of cIV at 2.5 μ g/ml, overnight at 29°C. The coated areas were "blocked" for two hours with BSA at 2 mg/ml, in PBS. Human

mesangial cells were processed as before, seeded on each spot of cIV in 50 μ l of binding buffer (2500 cells) and allowed to adhere for 5 hours at 37°C. The unbound cells were washed off with PBS. Adherent cells were fixed with 2% paraformaldehyde in HBSS for 30 minutes followed by permeabilization with 0.5% Triton X-100 for 2 minutes.

- 5 The cells were blocked again with PBS following which 200 μ l of hybridoma culture supernatant containing anti- α 1 antibody (TS1/7) was added to each spot and incubated at room temperature for 1 hour. The coverslips were then thoroughly washed and rhodamine-conjugated goat anti-mouse antibody (1:100) (Boehringer Mannheim, Indianapolis, IN) was added for one hour. The coverslips were again washed and
- 10 incubated with anti-vinculin antibodies (Sigma, St. Louis, MO) pre-conjugated (Quicktag, FITC labeling kit, Boehringer Mannheim, Indianapolis, IN) to FITC labeled goat anti-mouse antibody for 1 hour at room temperature. The coverslips were finally washed, mounted on glass slides and viewed for focal adhesions by co-localization of vinculin with α 1 integrin.

15

Staining of normal human adult kidneys for the presence of β 1 integrins

Normal human adult kidney tissue was snap frozen in liquid nitrogen and sections were prepared with a cryostat at 5 μ m intervals. The sections were stained using an anti-mouse Vectastain Elite Kit (as described by Wayner et al., 1993) with

20 diamino benzene (DAB) as the chromogen. The following mAbs were used: α 1 (TS2/7), α 2 (P1H5), α 3 (P3D11), α 4 (P4G9) and β 1 (P5D2). These monoclonal antibodies are available from the following sources and stained the following histological areas as was demonstrated in these studies:

- | | | |
|----|--------------------|--|
| 25 | α 1 (TS2/7) | Martin Hemler, Dana Farber Cancer Center, Boston, MA.
Stained mesangium. |
| | α 2 (P1H5) | EA Wayner, Fred Hutchinson Cancer Center, Seattle, WA
Stained mesangium. |
| 30 | α 3 (P3D11) | EA Wayner, Fred Hutchinson Cancer Center, Seattle, WA
Stained the mesangium,
endothelium, visceral and Bowman's
epithelium and capsule. |
| 35 | α 4 (P4G9) | EA Wayner, Fred Hutchinson Cancer Center, Seattle, WA
Did not stain glomeruli. |

β 1 (P5D2) EA Wayner, Fred Hutchinson Cancer Center, Seattle, WA
Stained mesangium, endothelium,
visceral epithelium, Bowman's
epithelium and capsule.

5

Normal mouse IgG (all isotypes) was used as a negative control.

These studies demonstrated the presence of α 1 β 1 and α 2 β 1 integrin receptors in focal adhesions. Focal adhesions are observed when cells spread in culture on matrix components such as collagen IV, fibronectin or laminin. Integrins cluster at the site of focal adhesions on the cell surface with intracellular fibers such as vinculin staining at these locations within the cell periphery. (see Hynes, et al. *Cell* 69:11-25, 1992 and Burridge, et al. *Ann. Rev. Cell Biol.* 4:487-525, 1988). This supports the hypothesis that mesangial cells use α 1 β 1 and α 2 β 1 integrin receptors to bind to cIV. It has been well established that when a particular integrin receptor is engaged by a specific ligand it can be detected in focal contacts co-localized with certain components of the cytoskeleton such as vinculin. Therefore, we asked whether mesangial cells could localize α 1 (or α 2 and β 1) to focal adhesions when seeded on cIV coated substrates.

α 2 or β 1 could be detected in focal contacts on cIV regardless of whether mesangial cells were grown in either low or high glucose. Additionally, when mesangial cells were grown in 5 mM glucose and subsequently seeded on cIV coated surfaces, α 1 could also be co-localized with vinculin within several focal contacts by dual-label immunofluorescence staining. It is believed that cIV binding in cells maintained in low glucose engages both the α 1 and α 2 subunits. α 1 could be detected in only some of the focal adhesions stained by vinculin. As a control, α 1 was not detected in focal contacts when mesangial cells were seeded onto fibronectin coated surfaces regardless of the glucose concentration of the cell culture media.

Immunohistochemical staining of integrin receptor subunits in normal human adult and fetal kidney revealed that both α 1 and α 2 could be localized within the mesangium. The α 1 receptor was diffusely expressed throughout the mesangium whereas the distribution of α 2 was more limited and focal. Also consistent with the results we obtained with cultured mesangial cells, β 1 and α 3 were intensely expressed throughout the mesangium, while α 4 could not be detected in either fetal or adult mesangium.

Example 4
Alterations in RNA Production in Human Mesangial Cells
cultured in High and Low Glucose Concentrations

5 Our efforts have concentrated on finding a way to predict, at early stages after the onset of diabetes, the subjects who will later develop nephropathy. We focused on a major hallmark of diabetic nephropathy, that of mesangial expansion. We first examined mesangial cells in culture, since these cells secrete their surrounding matrix, which is expanded in diabetes; however, biopsied tissue can be treated in the same
10 manner, as will be understood by those skilled in the art. The matrix consists primarily of collagen IV.

 Primary cultures of human mesangial cells undergo several phenotypic changes in response to elevated glucose concentrations and glucose-modified ("glycated") collagen IV. These changes included altered cell interactions with the collagen matrix.
15 In elevated glucose concentrations, the $\alpha 1$ subunit underwent a substantial decrease, concomitant with an increase of the $\alpha 2$ integrin subunit. This change was observed with immunoprecipitation and flow cytometry. Further studies with Northern analysis and *in situ* hybridization of the cultured mesangial cells confirmed the integrin reversal. In the studies employing Northern analyses, separate samples of total RNA were isolated from
20 the mesangial cells on each culture plate or alternatively from rat kidneys (see Example 5, below) by a single-step method using RNA STAT-60TM isolation reagent (TEL-TEST "B", INC., Friendswood, TX) according to the manufacturers directions. Briefly, the cells were lysed with RNA STAT-60TM solution by repetitive pipetting; the tissues were cut into small pieces and homogenized in the RNA STAT-60 solution with a high-speed
25 tissue homogenizer (Polytron CH6005, Luzern, Switzerland). The nucleic acid mixture was extracted with 0.2 ml chloroform per 1ml of the RNA STAT-60TM solution. Total RNA was precipitated for 10 min at -80°C in isopropanol, and the pelleted RNA was redissolved in TE buffer. The total RNA was free of DNA and proteins and had a 260/280 wavelength ratio > 1.8.

30 *Northern blot analysis*-The RNA samples were denatured in formaldehyde gel-running buffer (20 mM MOPS, 8 mM sodium acetate, mM EDTA, at pH 7.0) containing 6% formaldehyde and 50% formamide by heating at 65°C for 15 min. For each sample 20 mg of RNA was mixed with 6x loading buffer (50% glycerol, 1 mM

EDTA, 0.25% bromphenol blue, 0.25% Xylene cyanol FF), loaded on a 1% agarose gel submerged in 6% formaldehyde running buffer, and run at 3-5 V/cm for 3-4 hours. RNA was transferred from the agarose gel to a nylon membrane (Boehringer Mannheim, Indianapolis, IN) by capillary elution and immobilized by UV cross-linking (Stratalinker UV; Stratagene, La Jolla, CA). The membranes were then incubated in prehybridization solution containing 50% formamide, 5xSSC, 0.02% SDS, 0.1% N-lauroylsarcosine, 2% blocking reagent (Boehringer Mannheim), and 20 mM sodium maleate (pH 7.5) for >3 hours at 42°C. Radiolabeled probes (see Example 5) for the integrin subunits or controls were then added to the prehybridization solution and hybridization was performed overnight at 42°C (for cDNA probe) or 50°C (for antisense RNA probe). After hybridization, the membranes were initially washed in 2x SSC, 0.05% SDS for 10 minutes at room temperature and then washed for an additional 40 minutes at 42°C (for cDNA probe) or 60°C (for antisense RNA probe). Membranes were then exposed to X-ray film (X-Omat RP; Eastman Kodak Co., Rochester, NY) for 1 day at -80°C. After being stripped of previous probes by heating in 0.2x SSC, 0.5% SDS for 10 min at 100°C, the membranes were reprobed as described above. Images of autoradiograms were captured and digitized using a CCD video camera module interfaced with a microcomputer (Macintosh IICx; Apple Computers Inc., Cupertino, CA) and analyzed using image processing software (NIH Image 1.55b77: public domain).

Cells grown in 25 mM glucose expressed lower levels of $\alpha 1$ integrin than seen in an equivalent amount of RNA from cells grown in 5 mM glucose. Densitometric analysis demonstrated an $\approx 30\%$ decrease upon averaging the values from four samples. Similar analysis demonstrated $\approx 30\%$ increase in $\alpha 2$ integrin expression in cells grown in 25 mM glucose.

Example 5
***In Situ* Hybridization Detecting Expression of Integrins**
in Kidney Sections Taken at Various Times
After Onset of Diabetes

The expression of $\alpha 1$ and $\alpha 2$ integrin receptors was examined in rat kidney sections after the onset of diabetes.

The *in situ* hybridization approach was used to examine kidney sections of streptozotocin-diabetic rats, 2.5 months after induction of diabetes. At this time interval, glomerular changes were still minimal. The streptozotocin-induced diabetic rat model mimics human changes of mesangial expansion and glomerular basement
5 membrane thickening in late nephropathy and is an art accepted model for diabetes and nephropathy.

Female non-pregnant Sprague-Dawley rats were obtained from Brithwood, Minneapolis, MN. The animals weighed 190-210 g at the beginning of the experiments and were given a 52mg/kg intraperitoneal dose of streptozotocin (STZ, Zanazar brand,
10 Upjohn Corp., Kalamazoo, MI) in calcium citrate and calcium carbonate Buffer (pH 4.5) to induce diabetes, while the controls were injected with the same amount of Hanks' balanced salt solution (pH 7.2). The animals were fed on standard rat chow (Purina laboratory chow # 5001. RFG PET@Supply Company, Plymouth, MN), and tap water *ad libitum*. Presence of diabetes was confirmed by detection of >400mg/dl nonfasting
15 plasma glucose levels 10 days post injection by tail vein bleeding using the glucose peroxide method (Beckman glucose analyzer, Beckman Instruments, Inc., Fullerton, CA).

Body weight was determined weekly, blood glucose levels were determined at 4 weeks after induction of diabetes, and on the day before the termination of the
20 experiment, which was 2.5 month from induction of diabetes. Urinary albumin excretion (UAE) was determined by radial immunodiffusion Mancini method, using goat IgG fraction against rat albumin (Cappel Cat. No. 55727) and purified rat albumin (Cappel Cat. No. 55952, Cappel Research Products, Durham, NC), according to previously published procedures (Mauer et al, *Diabetes* 27:959-64, 1978). Rats were
25 sacrificed at 2.5 months after diabetes induction and kidney tissue was perfusionally fixed by injecting freshly prepared 4% paraformaldehyde through the renal artery. This was followed by overnight fixation in 4% paraformaldehyde after removal from the body. The tissue was sectioned at 5 μ m and placed on the silane-coated slides (Digene Diagnostics, Inc., Beltsville, MD) for *in situ* hybridization with probes for the α 1 and α 2
30 integrin subunits.

2.5 months after injection of STZ, diabetic rats weighted significantly less than controls, whereas their right kidney weight and serum glucose concentration were

significantly increased, as compared to the controls (see Table 1). Diabetic and non-diabetic rats demonstrated no significant difference in glomerular size and albumin excretion at 2.5 month after induction of diabetes (Table 1).

TABLE 1

TISSUE	CONTROL	DIABETIC	S/NS
Body Wt.(g)	390+/-10	200+/-20	S
Right Kidney wt. (g)	1.35+/-0.1	1.8+/-0.1	S
Plasma glucose (mg/dl)	140+/-25	760+/-150	S
Glomerular area	1.42+/-0.5	1.45+/-0.6	NS

5

A 5.4 kb human $\alpha 2$ integrin cDNA clone (Takada, et al., 1989, *supra*) and a rat $\alpha 1$ integrin cDNA clone (Ignatius et al, *supra*) in bluescript vector (Stratagene, La Jolla, CA) were used in these experiments. A 1.79 kb $\alpha 2$ integrin cDNA fragment was restriction digested from the EcoRI site. Similarly, a 3.98 kb $\alpha 1$ integrin cDNA fragment was obtained by restriction digestion from the EcoRI site.

10

cDNA fragments were purified by GENE CLEAN II kit (BIO 101, San Diego, CA) and labeled using the random primer labeling kit (Boehringer Mannheim, Indianapolis, IN) with P^{32} -dCTP (NEN) for Northern blotting and with S^{35} -dCTP (NEN) for *in situ* hybridization. GAPDH and sheep visna virus cDNA (PLV-KS) (Staskus et al, *Virology* 181:228-240, 1991) probes were used as the positive and negative controls respectively. The probes preferably had a specific activity of 2×10^8 - 1×10^9 dpm/ μ g.

15

By Northern blotting, compared to the controls, the diabetic kidneys expressed 113.5% more $\alpha 1$ (IV) RNA, 46.5% more $\alpha 3$ (IV) RNA, 54.8% less metalloproteinase-2 RNA (MMP-2, an enzyme that cleaves type IV collagen) and 246% more TIMP-1 RNA (a tissue inhibitor of metalloproteinases) with a $p < 0.01$ in all cases as determined by ANOVA.

20

The expression of $\alpha 1$ and $\alpha 2$ integrin RNA was localized using a modification of a previously described method for *in situ* hybridization (Staskus et al. *supra*). 5 μ m tissue sections on silane-coated slides were fixed in the freshly prepared 4% paraformaldehyde for 10 min. The slides were pretreated with 0.2N HCl for 20 min, 0.15 M Triethanolamine (TEA, Sigma, St. Louis, MO) for 15 min, 0.005% digitonin for 5 min, 3 mg/ml proteinase K (Sigma) for 15 min at 37°C, and 0.3% acetic anhydride -

25

O.1M TEA for 10 min. Hybridizations were performed under stringent hybridization conditions. Stringent hybridization conditions are defined in this specification as 50°C overnight, in 50% formamide, 0.6 M NaCl, 1x Denhardt's solution, 0.17 mg/ml human COT^{RT} DNA (GIBCO/BRL), 1 mg/ml poly A (Boehringer Mannheim), 10% (w/v) Dextran sulfate (Sigma), 0.1 M dithiothreitol (DTT, Boehringer Mannheim), 1 mM EDTA, 0.1 mM aurintricarboxylic acid (ATA, Sigma) and S³⁵-dCTP labeled cDNA probe. The next day, the slides were washed in 2x SSC-0.05% SDS for 60 min at 55°C (recipes for SSC and the like can be found in Sambrook, et al., *supra*); further washed in a high stringency washing buffer containing 50% formamide, 0.6 M NaCl, 1 mM EDTA, 5 mM DTT and 10 mM Hepes for 4 days at room temperature. After a brief rinse in 2x SSC, the slides were dehydrated in graded ethanol with 0.3 M ammonium acetate then dipped in Kodak NTB-2 emulsion and exposed for 5 days at 4°C.

After development the slides were stained with hematoxylin-eosin (Surgipath Canada, Inc., Winnipeg, Canada) and mounted. A ratio of the number of silver grains per cell was used to quantitate the results of *in situ* hybridization. Twenty glomeruli each were counted from each control and diabetic animal. Each glomerulus was assessed for: 1) glomerular area; 2) glomerular perimeter; 3) grains per glomerulus; and 4) number of cell nuclei per glomerulus.

The results were estimated as grains per cell nucleus and grains per glomerular area, as mean \pm SD of 5 animals (20 glomeruli each). (Haase, A.T., [1990]: *In situ* hybridization, CRC Press, 199-217; Nuovo, G.J., [1992] *PCR in situ* hybridization, protocols and applications, Raven Press). Groups were compared with the 2-tailed student t-test. Differences between groups were considered significant at $p < 0.05$.

The results are illustrated in Fig. 1. Early after induction of experimental diabetes, the expression of the $\alpha 1$ integrin subunit by glomerular cells was decreased compared to the control, whereas the expression of $\alpha 2$ integrin was increased. The average counts, in diabetic glomeruli hybridized with the $\alpha 1$ integrin probe, were significantly lower than control (Fig. 1). Also, the average counts, in diabetic glomeruli hybridized with the $\alpha 2$ integrin probe, were significantly higher than control (Fig. 1).

Control animals at 2.5 month diabetes expressed on an average a significantly higher level of $\alpha 1$ subunit integrin and significantly lower levels of $\alpha 2$ subunit integrin using unbiased methods of selection of areas for study. The entire section was surveyed

for RNA grains, the regions of the Bowman's space and the background count were excluded by studying a commensurate area of the negative control stained tissue.

Compared to the control, glomerular cells (GC:endothelial, epithelial and mesangial combine) and/or tubular (proximal and distal epithelial) cells (TC) had 36% (GC) less grains for $\alpha 1$ integrin; 86.4% (GC) more grains for $\alpha 2$ integrin; 82(TC)-167% (GC) more grains for $\alpha 1$ (IV); 107 (TC)-137% (GC) more grains for $\alpha 3$ (IV); 63.6(GC)-65.3%(TC) less MMP-2.

The results of the present study clearly demonstrate that mesangial cells, when cultured in high glucose (25 mM) instead of normal/low glucose (5 mM) alter their RNA production for the integrin subunits $\alpha 1$ and $\alpha 2$. Thus, this phenomenon is observed both at the level of protein and RNA production.

Furthermore, the results of our *in situ* hybridization and immunohistochemical staining experiments show that these changes can be detected in the mesangium of diabetic rat kidney and that human $\alpha 2$ integrin subunit probes and rat $\alpha 1$ integrin subunit probes are functional in both rat and human cells. Work by Mendrick and co-workers (*Lab. Invest.* 72(3):367-375, 1995) has shown that in the rat both integrins $\alpha 1\beta 1$ and $\alpha 2\beta 1$ of mesangial cells interact with collagen; as happens in the human mesangial cells. In the present study, the distribution of $\alpha 1$ and $\alpha 2$ integrin receptor subunit RNA was precisely localized by *in situ* hybridization to the different cell types of the glomerulus and surrounding tubules. Normal rat tissues expressed levels of the $\alpha 1$ subunit and also the $\alpha 2$ subunit RNA, as determined by counting the number ratio of silver grains/cell. However, the streptozotocin-induced diabetic animals had significantly lower levels of RNA for the $\alpha 1$ subunit and significantly higher levels of $\alpha 2$ subunit. A similar distribution of $\alpha 1$ and $\alpha 2$ subunit RNA (silver grains) was seen in the proximal and distal tubular epithelial cells. These data indicate that the distribution of cell surface integrin expression may be regulated by gene expression at the transcriptional level.

In summary, using *in situ* hybridization, similar results were seen in both mesangial cells *in vitro* and in glomeruli from tissue sections probed for the $\alpha 1$ and $\alpha 2$ integrin.

Early after induction of streptozotocin-diabetes in rates, substantial matrix-related gene expression changes occurred. For example, $\alpha 1$ and $\alpha 2$ integrin levels

changes, components of $\alpha 1\beta 1$ and $\alpha 2\beta 1$ integrin cell receptors for tIV (an important component of the renal extracellular matrix) underwent a reversal in levels with less $\alpha 1$ and more $\alpha 2$ integrin being present in glomeruli from kidneys of diabetic rats, when compared to the control. Expression of tIV was increased whereas the expression of MMP-2 which degrades tIV was substantially decreased. TIMP-1, an inhibitor of MMP-2 was increased. The observed matrix changes indicate an imbalance of tIV synthesis and turnover. This dysmetabolism of tIV, apparent in both the glomerular and tubular areas of the kidney, occurred before significant renal functional changes, or matrix accumulation out of proportion to renal enlargement, could be detectable. These changes could have a regulatory role in significant basement membrane thickening and mesangial expansion of diabetic nephropathy.

Collectively, the obtained data indicate that increased glucose concentration induces quantitative changes in receptor synthesis and cell surface integrin expression of human mesangial cells. In the diabetic, all cell systems are exposed to hyperglycemia and it is known that many cell and organ systems are affected by the disease; therefore, other cell types could similarly be used to assess changes in the levels of $\alpha 1$ and/or $\alpha 2$ integrin subunit expression as a measure of a predisposition to a variety of diabetic-induced pathologies. Kyu-Jin, et al. (*supra*) have noted alterations in integrin subunit expression in skin fibroblasts of diabetic patients. This information, in conjunction with the data discussed herein, indicates that altered levels of integrin subunit expression can be detected from a variety of integrin-expressing cells in diabetic nephropathy patients.

These results support the *in vitro* primary human mesangial cell culture data demonstrating that changes in cell surface integrin expression indicate the onset of nephropathic changes.

Example 6

Detection of Altered Levels of $\alpha 1$ and $\alpha 2$ Integrin Subunit Expression in Humans using Blood and Tissue Samples

Patients with insulin-dependent diabetes mellitus (IDDM), individuals at risk for developing IDDM, patients with clinical diabetes nephropathy and healthy age matched volunteers are selected for studies to confirm the presence of altered $\alpha 1$ and $\alpha 2$ integrin subunit expression in integrin-producing cells. Clinical diabetic nephropathy is defined by the presence of persistent proteinuria (urinary AER > 300 $\mu\text{g/day}$) in sterile urine of

patients with >10 yr duration of disease and concomitant retinopathy and is confirmed by the presence of classic glomerulosclerotic lesions on renal biopsy. Normal, nondiabetic individuals without a family history of hypertension serve as control subjects.

5 Patients were biopsied as follows: For skin biopsies, a biopsy is taken from the anterior surface of the left forearm by excision under local anaesthetic such as ethyl chloride, see Trevisan, et al. *Diabetes* 41:1239-45, 1992. The biopsy is optionally divided in half. With half of the tissue frozen immediately in liquid nitrogen and the other half placed in Hanks balanced salt solution. The frozen tissue is embedded in
10 paraffin and processed for *in situ* hybridization as has been described above. A portion of the intact tissue is preferably immediately minced and processed for RNA isolation using techniques described above. Remaining minced tissue is gently digested with trypsin to obtain a cell suspension, washed in media containing serum to remove trypsin and plated onto tissue culture dishes containing 10% FCS supplemented DMEM with
15 antibiotics.

Renal biopsies were obtained as follows. Patients should have normal blood pressures, normal coagulation values and platelet counts. Ultrasound was used to precisely localize the kidney. Ultrasound was also used to determine renal size, structural defects and post-void residual urine. Renal biopsies were performed on
20 sedated patients using the Franklin modified Vim-Silverman or Truecut needles available from surgical supply suppliers. The biopsy specimens were immediately examined under a dissecting microscope to ensure that adequate samples of glomeruli were present for subsequent studies to quantitate integrin levels. Biopsied tissue was sectioned and processed for *in situ* hybridization as described in Example 5. In one
25 example, renal samples from diabetic patients who did not show signs of microalbuminuria, but who had diabetic siblings with renal nephropathy were processed for *in situ* hybridization and PCR *in situ* hybridization. Renal samples from diabetic patients without a family history of nephropathy were also studied by PCR *in situ* hybridization to detect altered levels of integrin subunit expression.

30 PCR *in situ* hybridization is performed as follows. Sections are fixed as described in Example 5 and rinsed in RNase free water. The protocol used is that described by Nuovo, et al. (*Am. J. Surg. Pathol.* 17:683-690, 1993.) Cells are treated

with pepsin and DNase as described. cDNA synthesis is initiated by adding 10 μ l of a solution containing one or more of the following probes listed in a 5'-3' orientation with their SEQ ID NOS and their nucleic acid location on the respective integrin gene with reverse transcriptase (Perkin-ELmer, Norwalk, Conn.):

5

<u>α1 integrin primer</u>	SEQ ID NO	NA location
CCAGAGTCACTCTCACAGAG	5	2729-2748
CACAGCGTACACGTACACC	6	1991-2009
CACTTATAGACATCTCCAG	7	646-664

10

<u>α2 integrin primer</u>	SEQ ID NO	NA location
CATCCATGTTGATGTCTG	8	1733-1750
CATGTGATTCACCGTCAG	9	894-910
GCATATTGAATTGCTCCGAATGTG	10	801-826

15

The resulting cDNAs are subjected to amplification containing a 1 μ M concentration (each) of one or more of the above primers with a paired primer located 5' to the primers provided above. Those skilled in the art will recognize that a variety of other primers could also be used from the α 1 and α 2 integrin gene sequence to similarly perform PCR *in situ* hybridization. The preferred primers paired with the above primers are provided below.

20

<u>α1 integrin primer</u>	SEQ ID NO	NA location	SEQ ID Pair
GGCGTATGCACAACGCA	11	2261-2277	5
GCGACAGCTGACCAGTCAGCA	12	1509-1529	6
CACTCCTCCACAGCTCCT	13	251-268	7
<u>α2 integrin primer</u>	SEQ ID NO	NA location	SEQ ID Pair
ACATGTACTCACTGG	14	1593-1608	8
CTCACATGTGGTCCTCTG	15	433-451	9
GTCCTGTTGACCTATCCACTGC	16	296-319	10

25

30

35

The SEQ ID Pair in the above table refers to the paired primer that provides amplification of the sequence positioned between the primer pairs on the respective integrin gene. The PCR products are detected by using an antidigoxigenin-alkaline phosphatase conjugate and the chromagen nitroblue tetrazolium (NBT)-5-bromo-4-chloro-3-indoylphosphate toluidinium (Salt) (BCIP). The counterstain nuclear fast red

is used to stain nuclei. Internal probes located within the nucleic acid regions amplified by PCR can also be used to identify the amplified fragments. Thus, based on the pairings provided above, oligonucleotide probes can be selected between regions 267-645, 1530-1990 and between 2278-2728 for the $\alpha 1$ integrin gene and between regions 320-800, 452-893, 1607-1732 for the $\alpha 2$ integrin gene and hybridized and stained following the *in situ* hybridization methods detailed in Example 5.

A blood sample is also taken from the patient and leukocytes are isolated from blood by centrifugation, followed by hypotonic shock of residual blood cells. The leukocytes are then processed for *in situ* hybridization as has been discussed in the preceding examples.

Results:

PCR *in situ* hybridization with renal tissues demonstrated decreased $\alpha 1$ and increased $\alpha 2$ integrin subunits in the patient with diabetic neuropathy as compared with control tissue.

Quantitative analysis of RNA grains per unit area of kidney glomeruli and tubules was performed by counting silver grains under epi-polarized light.

As shown in Table 2, both glomeruli and tubules of the diabetic neuropathy patient showed significantly decreased $\alpha 1$ integrin levels as compared to the control, whereas $\alpha 2$ integrin levels were significantly increased as compared with control levels.

TABLE 2

Sample	Glomeruli ^a		Tubules ^a	
	$\alpha 1$	$\alpha 2$	$\alpha 1$	$\alpha 2$
Control	156	83	136	101
Diabetic Neuropathy	121 ^b	95 ^c	89 ^c	124 ^b

^a = grains per unit area ^b = p < 0.05 ^c = p < 0.01

These results confirm the *in vitro* observations in mesangial cells that there is a decrease of the $\alpha 1$ integrin subunit and a concomitant increase of $\alpha 2$ integrin

expression in a diabetic nephropathy. This represents a reversal of mesangial integrins which mediate binding of mesangial cells to collagen IV.

Example 7

Increased Integrin Subunit Expression in Skin Fibroblasts From Diabetic Patients with Nephropathy as Compared with Control Diabetic Patients

Fibroblasts were obtained from skin biopsies from diabetic patients with or without diabetic nephropathy and cultured as described for Example 6. Expression of $\alpha 3$, $\alpha 5$, and beta-1 integrin subunits in the cultured cells was analyzed by Northern blotting and subsequent densitometry, as described above, and using published probes.

For the $\alpha 3$ integrin subunit, the 1.9 Sall fragment described in Takada Y., et al., *J. Cell Biol.* 115:257-266 was used. For the $\beta 1$ subunit, the 3.6 kb insert of the $\beta 1$ subunit (the whole cDNA), described in Giancotti and Ruoslahti, *Cell* 60:849-850 (1990) was used. For the $\alpha 5$ subunit, the 3.7 kb Sall-Xba insert of the $\alpha 5$ subunit (the whole cDNA) described in Giancotti and Ruoslahti, *Supra* as used. These probes were radiolabeled and used under the same conditions as those described for Example 6.

The study included five patients per group, five each from the normal, diabetic "slow track" and from the Diabetic "fast track". Both groups of diabetic human subjects had renal function studies and kidney biopsies performed as part of their evaluation as possible candidates for pancreas transplantation. All procedures were approved by the Committee on Human Subjects at the University of Minnesota, and all patients gave written consent. All patients spent one week at the Clinical Research Center (CRC) at the University of Minnesota for pre-pancreas transplant evaluation, during which time they underwent multiple 24-hour urine collections (at least three) for measurements of creatinine clearance and urinary albumin excretion. Blood pressure was measured repeatedly by the CRC nursing staff. HbA1 was used to assess glycemic control. All patients underwent percutaneous kidney biopsy and skin biopsy. Patients were divided into two groups based on criteria of severity of renal lesions determined by morphometric analysis of mesangial functional volume and IDDM duration.

"Normal" samples were kidney biopsies from non-diabetic human subjects, taken to examine for the presence of neoplastic tissue, etc., on which a similar analysis to that performed for the diabetic tissues was done. These subjects underwent similar

renal functional studies to make certain that albuminuria, increased creatinine clearance, or hypertension were not present.

The data, shown below in Table 3, demonstrate a significant increase in $\alpha 3$ and beta-1 subunit expression in the skin fibroblasts of diabetic nephropathy patients as compared with the control diabetic patients.

TABLE 3

Integrin Subunit	Normal Values	Control Diabetic	Nephropathy Diabetics	p
$\alpha 3$	11.5 (9.1-13.3)	10.1 (8.6-12.8)	17.1 (16.1-35.6)	<0.5
$\alpha 5$	36.2 (18.3-46.6)	38.7 (31.6-57.2)	30.3 (13.2-48.4)	
b1	29.9 (24.0-33.4)	24.9 (17.4-30.9)	37.1 (24.2-74.6)	<0.5

While particular embodiments of the invention have been described in detail, it will be apparent to those skilled in the art, that these embodiments are exemplary rather than limiting, and the true scope of the invention is that defined in the following claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Regents of the University of Minnesota
- (ii) TITLE OF THE INVENTION: ANALYSIS OF ALPHA INTEGRINS
FOR THE DIAGNOSIS OF DIABETIC NEPHROPATHY
- (iii) NUMBER OF SEQUENCES: 16
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Merchant & Gould
 - (B) STREET: 3100 Norwest Center
90 South 7th Street
 - (C) CITY: Minneapolis
 - (D) STATE: MN
 - (E) COUNTRY: US
 - (F) ZIP: 55402
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ Version 1.5
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: Unknown
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Kettelberger, Denise
 - (B) REGISTRATION NUMBER: 33,924
 - (C) REFERENCE/DOCKET NUMBER: 600.314USWO
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 612-332-5300
 - (B) TELEFAX: 612-332-9081
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3987 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 420...3959

(A) NAME/KEY: mat_peptide

(B) LOCATION: 504

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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CCCGTGGACT TTAGCCTAAA CAGGGTCCCG CGAAGTTGGC TTTATTTGTC CATGTCTCGG      120
ACACAGCCTG GGTAGCTGCC ACTGAGATTT CAGGGACGGA GCGCGCAAAG GGGGGGGAAA      180
TGTGGCAATC CATCTGGGAT GTGAGACGCG TGGAGAGGGC TTAGCAGCAT TTGACCAAAA      240
CACAGGAAAT CACTCCTCCA CAGCTCCTGG GCGCAGCAGC GGCTGGGGCC ACTGCCGGAC      300
ACCCTCGGAG ACCACACGAG TGACCCAGAG CGCAAGTCGC CAGCGTCCCG GTTCTGCCTG      360
TTCCTGCCAG CTCCTGCCCA CGAACC GGCA CGTAGCTGTT TCCAGCAGCC GCTCCAGCA      419

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ATG GTC CCC AGG CGT CCT GCC AGC CTA GAG GTC ACT GTA GCC TGC ATA      467
Met Val Pro Arg Arg Pro Ala Ser Leu Glu Val Thr Val Ala Cys Ile
-28          -25          -20          -15

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TGG CTT CTC ACG GTC ATC CTA GGC TTC TGC GTC TCC TTC AAT GTT GAT      515
Trp Leu Leu Thr Val Ile Leu Gly Phe Cys Val Ser Phe Asn Val Asp
-10          -5          1

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GTG AAA AAC TCA ATG AGT TTC AGT GGC CCA GTA GAG GAC ATG TTT GGA      563
Val Lys Asn Ser Met Ser Phe Ser Gly Pro Val Glu Asp Met Phe Gly
5          10          15          20

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TAC ACT GTT CAA CAA TAT GAA AAC GAA GAA GGC AAA TGG GTT CTT ATT      611
Tyr Thr Val Gln Gln Tyr Glu Asn Glu Glu Gly Lys Trp Val Leu Ile
25          30          35

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GGT TCT CCT TTA GTT GGC CAA CCC AAA GCA AGA ACT GGA GAT GTC TAT      659
Gly Ser Pro Leu Val Gly Gln Pro Lys Ala Arg Thr Gly Asp Val Tyr
40          45          50

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AAG TGT CCG GTT GGG AGA GAG AGA GCA ATG CCT TGC GTG AAG TTG GAC      707
Lys Cys Pro Val Gly Arg Glu Arg Ala Met Pro Cys Val Lys Leu Asp
55          60          65

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TTG CCA GTT AAC ACA TCG ATC CCC AAT GTC ACA GAA ATA AAG GAA AAC	755
Glu Pro Val Asn Thr Ser Ile Pro Asn Val Thr Glu Ile Lys Glu Asn	
70 75 80	
ATG ACA TTT GGA TCA ACT TTA GTC ACC AAC CCG AAT GGA GGA TTT CTG	803
Met Thr Phe Gly Ser Thr Leu Val Thr Asn Pro Asn Gly Gly Phe Leu	
85 90 95 100	
GCA TGT GGG CCC TTG TAT GCC TAT AGA TGT GGA CAT TTG CAT TAT ACA	851
Ala Cys Gly Pro Leu Tyr Ala Tyr Arg Cys Gly His Leu His Tyr Thr	
105 110 115	
ACT GGA ATA TGT TCT GAT GTC AGT CCT ACA TTT CAA GTT GTG AAC TCC	899
Thr Gly Ile Cys Ser Asp Val Ser Pro Thr Phe Gln Val Val Asn Ser	
120 125 130	
TTT GCC CCT GTA CAA GAA TGC AGC ACC CAG CTG GAC ATA GTC ATC GTC	947
Phe Ala Pro Val Gln Glu Cys Ser Thr Gln Leu Asp Ile Val Ile Val	
135 140 145	
CTG GAT GGC TCC AAC AGC ATC TAC CCC TGG GAA AGT GTC ATC GCC TTT	995
Leu Asp Gly Ser Asn Ser Ile Tyr Pro Trp Glu Ser Val Ile Ala Phe	
150 155 160	
TTA AAC GAC CTT CTT AAG AGG ATG GAT ATT GGC CCT AAG CAG ACA CAG	1043
Leu Asn Asp Leu Leu Lys Arg Met Asp Ile Gly Pro Lys Gln Thr Gln	
165 170 175 180	
GTC GGG ATT GTA CAG TAT GGA GAG AAT GTA ACC CAT GAG TTC AAC CTC	1091
Val Gly Ile Val Gln Tyr Gly Glu Asn Val Thr His Glu Phe Asn Leu	
185 190 195	
AAT AAG TAT TCA TCC ACA GAA GAG GTC CTT GTC GCA GCA AAC AAA ATA	1139
Asn Lys Tyr Ser Ser Thr Glu Glu Val Leu Val Ala Ala Asn Lys Ile	
200 205 210	
GGC CGA CAG GGA GGC CTC CAA ACG ATG ACA GCC CTT GGA ATA GAC ACA	1187
Gly Arg Gln Gly Gly Leu Gln Thr Met Thr Ala Leu Gly Ile Asp Thr	
215 220 225	
GCC AGG AAA GAG GCA TTC ACT GAA GCT CGG GGT GCC AGG AGG GGA GTT	1235
Ala Arg Lys Glu Ala Phe Thr Glu Ala Arg Gly Ala Arg Arg Gly Val	
230 235 240	
AAA AAA GTC ATG GTT ATT GTG ACC GAC GGA GAA TCG CAT GAC AAC TAT	1283
Lys Lys Val Met Val Ile Val Thr Asp Gly Glu Ser His Asp Asn Tyr	
245 250 255 260	
CGC TGA AAC AGG TCA TCC AAG ACT GCG AGG ACG AAA ACA TTC AGC GAT	1331
Arg Leu Lys Gln Val Ile Gln Asp Cys Glu Asp Glu Asn Ile Gln Arg	
265 270 275	
TTT TCC ATA GCT ATC CTT GGC CAC TAT AAC AGG GGG AAC TTA AGC ACT	1379
Phe Ser Ile Ala Ile Leu Gly His Tyr Asn Arg Gly Asn Leu Ser Thr	
280 285 290	

GAA Glu	AAA Lys	TTT Phe	GTG Val	GAG Glu	GAA Glu	ATA Ile	AAA Lys	TCG Ser	ATC Ile	GCA Ala	AGC Ser	GAG Glu	CCC Pro	ACG Thr	GAA Glu	1427
		295					300					305				
AAG Lys	CAC His	TTC Phe	TTC Phe	AAT Asn	GTC Val	TCG Ser	GAT Asp	GAG Glu	TTG Leu	GCC Ala	CTG Leu	GTC Val	ACT Thr	ATT Ile	GTT Val	1475
		310					315					320				
AAA Lys	GCT Ala	CTG Leu	GGA Gly	GAA Glu	AGG Arg	ATA Ile	TTC Phe	GCT Ala	TTG Leu	GAA Glu	GCG Ala	ACA Thr	GCT Ala	GAC Asp	CAG Gln	1523
		325					330					335				340
TCA Ser	GCA Ala	GCT Ala	TCA Ser	TTT Phe	GAG Glu	ATG Met	GAA Glu	ATG Met	TCT Ser	CAG Gln	ACT Thr	GGC Gly	TTC Phe	AGT Ser	GCT Ala	1571
				345					350					355		
CAC His	TAC Tyr	TCC Ser	CAG Gln	GAC Asp	TGG Trp	GTC Val	ATG Met	CTT Leu	GGA Gly	GCG Ala	GTG Val	GGA Gly	GCC Ala	TAT Tyr	GAC Asp	1619
				360					365					370		
TGG Trp	AAC Asn	GGA Gly	ACT Thr	GTG Val	GTC Val	ATG Met	CAG Gln	AAG Lys	GCT Ala	AAC Asn	CAG Gln	ATG Met	GTC Val	ATC Ile	CCT Pro	1667
				375					380					385		
CAT His	AAC Asn	ACC Thr	ACC Thr	TTT Phe	CAA Gln	ACT Thr	GAG Glu	CCC Pro	GCC Ala	AAG Lys	ATG Met	AAC Asn	GAG Glu	CCT Pro	CTG Leu	1715
				390					395					400		
GCT Ala	TCT Ser	TAT Tyr	TTA Leu	GGT Gly	TAC Tyr	ACA Thr	GTG Val	AAC Asn	TCG Ser	GCC Ala	ACC Thr	ATC Ile	CCT Pro	GGA Gly	GAT Asp	1763
				405					410					415		
GTG Val	CTC Leu	TAC Tyr	ATC Ile	GCT Ala	GGG Gly	CAG Gln	CCT Pro	CGG Arg	TAC Tyr	AAT Asn	CAT His	ACG Thr	GGC Gly	CAG Gln	GTC Val	1811
				425					430					435		
GTC Val	ATC Ile	TAC Tyr	AAG Lys	ATG Met	GAG Glu	GAT Asp	GGG Gly	AAC Asn	ATC Ile	AAC Asn	ATT Ile	CTG Leu	CAG Gln	ACA Thr	CTC Leu	1859
				440					445					450		
GGC Gly	GGA Gly	GAG Glu	CAG Gln	ATT Ile	GGT Gly	TCC Ser	TAC Tyr	TTT Phe	GGT Gly	AGT Ser	GTC Val	TTA Leu	ACA Thr	ACA Thr	ATT Ile	1907
				455					460					465		
GAC Asp	ATC Ile	GAC Asp	AAA Lys	GAT Asp	TCT Ser	TAT Tyr	ACT Thr	GAT Asp	CTG Leu	CTT Leu	CTC Leu	GTC Val	GGG Gly	GCC Ala	CCC Pro	1955
				470					475					480		
ATG Met	TAC Tyr	ATG Met	GGG Gly	ACA Thr	GAG Glu	AAA Lys	GAG Glu	GAA Glu	CAG Gln	GGC Gly	AAG Lys	GTG Val	TAC Tyr	GTG Val	TAC Tyr	2003
				485					490					495		
GCT Ala	GTG Val	AAT Asn	CAG Gln	ACA Thr	AGG Arg	TTT Phe	GAA Glu	TAT Tyr	CAA Gln	ATG Met	AGC Ser	CTG Leu	GAA Glu	CCA Pro	ATT Ile	2051
				505					510					515		

GGC AGA CCT GCT GCT CAT CCC TGA AGG ATA ATT CAT GCA CGA AAG AAA	2099
Arg Gln Thr Cys Cys Ser Ser Leu Lys Asp Asn Ser Cys Thr Lys Glu	
520 525 530	
AAC AAG AAT GAG CCC TGC GGG GCC CGC TTC GGA ACA GCA ATT GCT GCT	2147
Asn Lys Asn Glu Pro Cys Gly Ala Arg Phe Gly Thr Ala Ile Ala Ala	
535 540 545	
GTA AAA GAC CTC AAC GTG GAT GGA TTT AAT GAC GTC GTG ATT GGA GCT	2195
Val Lys Asp Leu Asn Val Asp Gly Phe Asn Asp Val Val Ile Gly Ala	
550 555 560	
CCG CTG GAA GAT GAC CAC GCA GGA GCT GTG TAC ATT TAT CAT GGC AGT	2243
Pro Leu Glu Asp Asp His Ala Gly Ala Val Tyr Ile Tyr His Gly Ser	
565 570 575 580	
GGC AAG ACC ATA AGG GAG GCG TAT GCA CAA CGC ATT CCA TCA GGT GGG	2291
Gly Lys Thr Ile Arg Glu Ala Tyr Ala Gln Arg Ile Pro Ser Gly Gly	
585 590 595	
GAT GGC AAG ACC CTG AAA TTT TTC GGC CAG TCT ATC CAC GGA GAG ATG	2339
Asp Gly Lys Thr Leu Lys Phe Phe Gly Gln Ser Ile His Gly Glu Met	
600 605 610	
GAT TTA AAT GGT GAC GGT CTG ACT GAC GTG ACC ATT GGA GGC CTT GGT	2387
Asp Leu Asn Gly Asp Gly Leu Thr Asp Val Thr Ile Gly Gly Leu Gly	
615 620 625	
GGA GCA GCC CTC TTC TGG GCC AGA GAT GTG GCT GTA GTT AAA GTG ACC	2435
Gly Ala Ala Leu Phe Trp Ala Arg Asp Val Ala Val Val Lys Val Thr	
630 635 640	
ATG AAT TTT GAA CCC AAT AAA GTG AAT ATT CAA AAG AAA AAC TGC CGT	2483
Met Asn Phe Glu Pro Asn Lys Val Asn Ile Gln Lys Lys Asn Cys Arg	
645 650 655 660	
GTG GAG GGC AAA GAA ACA GTG TGC ATA AAT GCT ACA ATG TGT TTT CAT	2531
Val Glu Gly Lys Glu Thr Val Cys Ile Asn Ala Thr Met Cys Phe His	
665 670 675	
GTG AAA TTA AAG TCT AAA GAG GAC TCA ATT TAC GAG GCT GAT CTG CAG	2579
Val Lys Leu Lys Ser Lys Glu Asp Ser Ile Tyr Glu Ala Asp Leu Gln	
680 685 690	
TAC CGT GTC ACC CTT GAT TCA CTG AGG CAG ATA TCA CGG AGC TTT TTT	2627
Tyr Arg Val Thr Leu Asp Ser Leu Arg Gln Ile Ser Arg Ser Phe Phe	
695 700 705	
TCT GGA ACT CAG GAA AGG AAG ATT CAA AGA AAT ATC ACC GTT CGA GAA	2675
Ser Gly Thr Gln Glu Arg Lys Ile Gln Arg Asn Ile Thr Val Arg Glu	
710 715 720	
TCA GAA TGC ATC AGG CAC TCC TTC TAC ATG TTG GAC AAA CAT GAC TTT	2723
Ser Glu Cys Ile Arg His Ser Phe Tyr Met Leu Asp Lys His Asp Phe	
725 730 735 740	

CAG GAC TCT GTG AGA GTG ACT CTG GAT TTT AAT CTC ACT GAT CCA GAA	2771
Gln Asp Ser Val Arg Val Thr Leu Asp Phe Asn Leu Thr Asp Pro Glu	
745 750 755	
AAT GGT CCT GTA CTT GAT GAC GCT CTG CCA AAC TCA GTC CAC GAA CAC	2819
Asn Gly Pro Val Leu Asp Asp Ala Leu Pro Asn Ser Val His Glu His	
760 765 770	
ATT CCC TTT GCC AAA GAC TGT GGA AAC AAG GAA AGA TGC ATT TCA GAC	2867
Ile Pro Phe Ala Lys Asp Cys Gly Asn Lys Glu Arg Cys Ile Ser Asp	
775 780 785	
CTC ACT CTG AAT GTG TCC ACC ACA GAA AAG AGC CTG CTG ATC GTC AAG	2915
Leu Thr Leu Asn Val Ser Thr Thr Glu Lys Ser Leu Leu Ile Val Lys	
790 795 800	
TCC CAG CAT GAC AAG TTC AAC GTT AGC CTC ACC GTC AAA AAC AAA GGA	2963
Ser Gln His Asp Lys Phe Asn Val Ser Leu Thr Val Lys Asn Lys Gly	
805 810 815 820	
GAC AGT GCG TAC AAC ACC AGG ACA GTG GTG CAG CAT TCA CCA AAT CTG	3011
Asp Ser Ala Tyr Asn Thr Arg Thr Val Val Gln His Ser Pro Asn Leu	
825 830 835	
ATT TTT TCG GGA ATT GAG GAG ATC CAA AAA GAT AGC TGT GAA TCT AAT	3059
Ile Phe Ser Gly Ile Glu Glu Ile Gln Lys Asp Ser Cys Glu Ser Asn	
840 845 850	
CAA AAT ATC ACT TGC AGA GTT GGA TAT CCT TTC CTA AGA GCA GGA GAA	3107
Gln Asn Ile Thr Cys Arg Val Gly Tyr Pro Phe Leu Arg Ala Gly Glu	
855 860 865	
ACG GTT ACC TTC AAA ATA ATA TTC CAG TTT AAC ACA TCC CAT CTC TCG	3155
Thr Val Thr Phe Lys Ile Ile Phe Gln Phe Asn Thr Ser His Leu Ser	
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GAA AAT GCA ATC ATT CAC TTA AGT GCA ACA AGT GAC AGT GAG GAG CCC	3203
Glu Asn Ala Ile Ile His Leu Ser Ala Thr Ser Asp Ser Glu Glu Pro	
885 890 895 900	
CTG GAA TCT CTT AAT GAT AAT GAA GTA AAT ATT TCC ATC CCA GTA AAA	3251
Leu Glu Ser Leu Asn Asp Asn Glu Val Asn Ile Ser Ile Pro Val Lys	
905 910 915	
TAT GAA GTT GGA CTG CAG TTT TAC AGT TCT GCG AGT GAA CAT CAC ATT	3299
Tyr Glu Val Gly Leu Gln Phe Tyr Ser Ser Ala Ser Glu His His Ile	
920 925 930	
TCA GTC GCT GCC AAT GAG ACG ATC CCT GAG TTT ATT AAC TCC ACT GAG	3347
Ser Val Ala Ala Asn Glu Thr Ile Pro Glu Phe Ile Asn Ser Thr Glu	
935 940 945	
GAC ATT GGG AAT GAA ATT AAT GTC TTC TAT ACG ATT AGA AAG AGG GGG	3395
Asp Ile Gly Asn Glu Ile Asn Val Phe Tyr Thr Ile Arg Lys Arg Gly	
950 955 960	

CAT TTC CCA ATG CCA GAA CTT CAG CTG TCA ATT TCA TTC CCC AAT TTG 3443
 His Phe Pro Met Pro Glu Leu Gln Leu Ser Ile Ser Phe Pro Asn Leu
 965 970 975 980

ACG GCA GAT GGT TAT CCT GTA CTG TAC CCA ATT GGA TGG TCA TCT TCA 3491
 Thr Ala Asp Gly Tyr Pro Val Leu Tyr Pro Ile Gly Trp Ser Ser Ser
 985 990 995

GAT AAT GTG AAC TGT AGA CCC CGG AGC CTT GAG GAC CCC TTT GGC ATC 3539
 Asp Asn Val Asn Cys Arg Pro Arg Ser Leu Glu Asp Pro Phe Gly Ile
 1000 1005 1010

AAC TCT GGG AAG AAA ATG ACA ATA TCG AAG TCT GAG GTT CTC AAA AGA 3587
 Asn Ser Gly Lys Lys Met Thr Ile Ser Lys Ser Glu Val Leu Lys Arg
 1015 1020 1025

GGC ACA ATC CAG GAC TGC AGT AGT ACG TGT GGA GTT GCC ACC ATC ACG 3635
 Gly Thr Ile Gln Asp Cys Ser Ser Thr Cys Gly Val Ala Thr Ile Thr
 1030 1035 1040

TGT AGC CTC CTT CCT TCC GAC CTG AGT CAA GTG AAT GTC TCG CTC CTC 3683
 Cys Ser Leu Leu Pro Ser Asp Leu Ser Gln Val Asn Val Ser Leu Leu
 1045 1050 1055 1060

CTG TGG AAA CCG ACT TTC ATA AGA GCA CAT TTT TCC AGC TTA AAC CTT 3731
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 1065 1070 1075

ACT CTA AGA GGA GAA CTT AAG AGT GAA AAT TCA TCG CTG ACT TTA AGT 3779
 Thr Leu Arg Gly Glu Leu Lys Ser Glu Asn Ser Ser Leu Thr Leu Ser
 1080 1085 1090

AGC AGC AAC CGG AAG CGA GAG CTG GCT ATT CAG ATA TCC AAA GAC GGG 3827
 Ser Ser Asn Arg Lys Arg Glu Leu Ala Ile Gln Ile Ser Lys Asp Gly
 1095 1100 1105

CTC CCA GGC AGA GTG CCG CTG TGG GTT ATC CTC CTG AGC GCC TTC GCG 3875
 Leu Pro Gly Arg Val Pro Leu Trp Val Ile Leu Leu Ser Ala Phe Ala
 1110 1115 1120

GGG CTA CTG CTG CTA ATG CTC CTT ATA TTG GCT CTG TGG AAG ATT GGA 3923
 Gly Leu Leu Leu Leu Met Leu Leu Ile Leu Ala Leu Trp Lys Ile Gly
 1125 1130 1135 1140

TTC TTC AAA AGG CCA CTG AAG AAG AAA ATG GAG AAA TGAAAGGTTT 3969
 Phe Phe Lys Arg Pro Leu Lys Lys Lys Met Glu Lys
 1145 1150

CATAGAAAAA AAAAAAAAAA 3987

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Val Pro Arg Arg Pro Ala Ser Leu Glu Val Thr Val Ala Cys Ile
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Trp Leu Leu Thr Val Ile Leu Gly Phe Cys Val Ser Phe Asn Val Asp
    -10          -5          1

Val Lys Asn Ser Met Ser Phe Ser Gly Pro Val Glu Asp Met Phe Gly
  5          10          15          20

Tyr Thr Val Gln Gln Tyr Glu Asn Glu Glu Gly Lys Trp Val Leu Ile
    25          30          35

Gly Ser Pro Leu Val Gly Gln Pro Lys Ala Arg Thr Gly Asp Val Tyr
    40          45          50

Lys Cys Pro Val Gly Arg Glu Arg Ala Met Pro Cys Val Lys Leu Asp
    55          60          65

Glu Pro Val Asn Thr Ser Ile Pro Asn Val Thr Glu Ile Lys Glu Asn
    70          75          80

Met Thr Phe Gly Ser Thr Leu Val Thr Asn Pro Asn Gly Gly Phe Leu
    85          90          95          100

Ala Cys Gly Pro Leu Tyr Ala Tyr Arg Cys Gly His Leu His Tyr Thr
    105          110          115

Thr Gly Ile Cys Ser Asp Val Ser Pro Thr Phe Gln Val Val Asn Ser
    120          125          130

Phe Ala Pro Val Gln Glu Cys Ser Thr Gln Leu Asp Ile Val Ile Val
    135          140          145

Leu Asp Gly Ser Asn Ser Ile Tyr Pro Trp Glu Ser Val Ile Ala Phe
    150          155          160

Leu Asn Asp Leu Leu Lys Arg Met Asp Ile Gly Pro Lys Gln Thr Gln
    165          170          175          180

Val Gly Ile Val Gln Tyr Gly Glu Asn Val Thr His Glu Phe Asn Leu
    185          190          195

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Asn Lys Tyr Ser Ser Thr Glu Glu Val Leu Val Ala Ala Asn Lys Ile
 200 205 210

Gly Arg Gln Gly Gly Leu Gln Thr Met Thr Ala Leu Gly Ile Asp Thr
 215 220 225

Ala Arg Lys Glu Ala Phe Thr Glu Ala Arg Gly Ala Arg Arg Gly Val
 230 235 240

Lys Lys Val Met Val Ile Val Thr Asp Gly Glu Ser His Asp Asn Tyr
 245 250 255 260

Arg Leu Lys Gln Val Ile Gln Asp Cys Glu Asp Glu Asn Ile Gln Arg
 265 270 275

Phe Ser Ile Ala Ile Leu Gly His Tyr Asn Arg Gly Asn Leu Ser Thr
 280 285 290

Glu Lys Phe Val Glu Glu Ile Lys Ser Ile Ala Ser Glu Pro Thr Glu
 295 300 305

Lys His Phe Phe Asn Val Ser Asp Glu Leu Ala Leu Val Thr Ile Val
 310 315 320

Lys Ala Leu Gly Glu Arg Ile Phe Ala Leu Glu Ala Thr Ala Asp Gln
 325 330 335 340

Ser Ala Ala Ser Phe Glu Met Glu Met Ser Gln Thr Gly Phe Ser Ala
 345 350 355

His Tyr Ser Gln Asp Trp Val Met Leu Gly Ala Val Gly Ala Tyr Asp
 360 365 370

Trp Asn Gly Thr Val Val Met Gln Lys Ala Asn Gln Met Val Ile Pro
 375 380 385

His Asn Thr Thr Phe Gln Thr Glu Pro Ala Lys Met Asn Glu Pro Leu
 390 395 400

Ala Ser Tyr Leu Gly Tyr Thr Val Asn Ser Ala Thr Ile Pro Gly Asp
 405 410 415 420

Val Leu Tyr Ile Ala Gly Gln Pro Arg Tyr Asn His Thr Gly Gln Val
 425 430 435

Val Ile Tyr Lys Met Glu Asp Gly Asn Ile Asn Ile Leu Gln Thr Leu
 440 445 450

Gly Gly Glu Gln Ile Gly Ser Tyr Phe Gly Ser Val Leu Thr Thr Ile
 455 460 465

Asp Ile Asp Lys Asp Ser Tyr Thr Asp Leu Leu Leu Val Gly Ala Pro
 470 475 480

Met Tyr Met Gly Thr Glu Lys Glu Glu Gln Gly Lys Val Tyr Val Tyr
 485 490 495 500

Ala Val Asn Gln Thr Arg Phe Glu Tyr Gln Met Ser Leu Glu Pro Ile
 505 510 515

Arg Gln Thr Cys Cys Ser Ser Leu Lys Asp Asn Ser Cys Thr Lys Glu
 520 525 530

Asn Lys Asn Glu Pro Cys Gly Ala Arg Phe Gly Thr Ala Ile Ala Ala
 535 540 545

Val Lys Asp Leu Asn Val Asp Gly Phe Asn Asp Val Val Ile Gly Ala
 550 555 560

Pro Leu Glu Asp Asp His Ala Gly Ala Val Tyr Ile Tyr His Gly Ser
 565 570 575 580

Gly Lys Thr Ile Arg Glu Ala Tyr Ala Gln Arg Ile Pro Ser Gly Gly
 585 590 595

Asp Gly Lys Thr Leu Lys Phe Phe Gly Gln Ser Ile His Gly Glu Met
 600 605 610

Asp Leu Asn Gly Asp Gly Leu Thr Asp Val Thr Ile Gly Gly Leu Gly
 615 620 625

Gly Ala Ala Leu Phe Trp Ala Arg Asp Val Ala Val Val Lys Val Thr
 630 635 640

Met Asn Phe Glu Pro Asn Lys Val Asn Ile Gln Lys Lys Asn Cys Arg
 645 650 655 660

Val Glu Gly Lys Glu Thr Val Cys Ile Asn Ala Thr Met Cys Phe His
 665 670 675

Val Lys Leu Lys Ser Lys Glu Asp Ser Ile Tyr Glu Ala Asp Leu Gln
 680 685 690

Tyr Arg Val Thr Leu Asp Ser Leu Arg Gln Ile Ser Arg Ser Phe Phe
 695 700 705

Ser Gly Thr Gln Glu Arg Lys Ile Gln Arg Asn Ile Thr Val Arg Glu
 710 715 720

Ser Glu Cys Ile Arg His Ser Phe Tyr Met Leu Asp Lys His Asp Phe
 725 730 735 740

Gln Asp Ser Val Arg Val Thr Leu Asp Phe Asn Leu Thr Asp Pro Glu
 745 750 755

Asn Gly Pro Val Leu Asp Asp Ala Leu Pro Asn Ser Val His Glu His
 760 765 770

Ile Pro Phe Ala Lys Asp Cys Gly Asn Lys Glu Arg Cys Ile Ser Asp
 775 780 785

Leu Thr Leu Asn Val Ser Thr Thr Glu Lys Ser Leu Leu Ile Val Lys
 790 795 800

Ser Gln His Asp Lys Phe Asn Val Ser Leu Thr Val Lys Asn Lys Gly
 805 810 815 820
 Asp Ser Ala Tyr Asn Thr Arg Thr Val Val Gln His Ser Pro Asn Leu
 825 830 835
 Ile Phe Ser Gly Ile Glu Glu Ile Gln Lys Asp Ser Cys Glu Ser Asn
 840 845 850
 Gln Asn Ile Thr Cys Arg Val Gly Tyr Pro Phe Leu Arg Ala Gly Glu
 855 860 865
 Thr Val Thr Phe Lys Ile Ile Phe Gln Phe Asn Thr Ser His Leu Ser
 870 875 880
 Glu Asn Ala Ile Ile His Leu Ser Ala Thr Ser Asp Ser Glu Glu Pro
 885 890 895 900
 Leu Glu Ser Leu Asn Asp Asn Glu Val Asn Ile Ser Ile Pro Val Lys
 905 910 915
 Tyr Glu Val Gly Leu Gln Phe Tyr Ser Ser Ala Ser Glu His His Ile
 920 925 930
 Ser Val Ala Ala Asn Glu Thr Ile Pro Glu Phe Ile Asn Ser Thr Glu
 935 940 945
 Asp Ile Gly Asn Glu Ile Asn Val Phe Tyr Thr Ile Arg Lys Arg Gly
 950 955 960
 His Phe Pro Met Pro Glu Leu Gln Leu Ser Ile Ser Phe Pro Asn Leu
 965 970 975 980
 Thr Ala Asp Gly Tyr Pro Val Leu Tyr Pro Ile Gly Trp Ser Ser Ser
 985 990 995
 Asp Asn Val Asn Cys Arg Pro Arg Ser Leu Glu Asp Pro Phe Gly Ile
 1000 1005 1010
 Asn Ser Gly Lys Lys Met Thr Ile Ser Lys Ser Glu Val Leu Lys Arg
 1015 1020 1025
 Gly Thr Ile Gln Asp Cys Ser Ser Thr Cys Gly Val Ala Thr Ile Thr
 1030 1035 1040
 Cys Ser Leu Leu Pro Ser Asp Leu Ser Gln Val Asn Val Ser Leu Leu
 1045 1050 1055 1060
 Leu Trp Lys Pro Thr Phe Ile Arg Ala His Phe Ser Ser Leu Asn Leu
 1065 1070 1075
 Thr Leu Arg Gly Glu Leu Lys Ser Glu Asn Ser Ser Leu Thr Leu Ser
 1080 1085 1090
 Ser Ser Asn Arg Lys Arg Glu Leu Ala Ile Gln Ile Ser Lys Asp Gly
 1095 1100 1105

Leu Pro Gly Arg Val Pro Leu Trp Val Ile Leu Leu Ser Ala Phe Ala
 1110 1115 1120

Gly Leu Leu Leu Leu Met Leu Leu Ile Leu Ala Leu Trp Lys Ile Gly
 1125 1130 1135 1140

Phe Phe Lys Arg Pro Leu Lys Lys Lys Met Glu Lys
 1145 1150

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 49...3591
- (D) OTHER INFORMATION:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 136
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTCCTGC AAACCCAGCG CAACTACGGT CCCCCGGTCA GACCCAGG ATG GGG CCA	57
Met Gly Pro	
-29	
GAA CGG ACA GGG GCC GCG CCG CTG CCG CTG CTG CTG GTG TTA GCG CTC	105
Glu Arg Thr Gly Ala Ala Pro Leu Pro Leu Leu Leu Val Leu Ala Leu	
-25 -20 -15	
AGT CAA GGC ATT TTA AAT TGT TGT TTG GCC TAC AAT GTT GGT CTC CCA	153
Ser Gln Gly Ile Leu Asn Cys Cys Leu Ala Tyr Asn Val Gly Leu Pro	
-10 -5 1 5	
GAA GCA AAA ATA TTT TCC GGT CCT TCA AGT GAA CAG TTT GGG TAT GCA	201
Glu Ala Lys Ile Phe Ser Gly Pro Ser Ser Glu Gln Phe Gly Tyr Ala	
10 15 20	
GTG CAG CAG TTT ATA AAT CCA AAA GGC AAC TGG TTA CTG GTT GGT TCA	249
Val Gln Gln Phe Ile Asn Pro Lys Gly Asn Trp Leu Leu Val Gly Ser	
25 30 35	

CCC TGG AGT GGC TTT CCT GAG AAC CGA ATG GGA GAT GTG TAT AAA TGT	297
Pro Trp Ser Gly Phe Pro Glu Asn Arg Met Gly Asp Val Tyr Lys Cys	
40 45 50	
CCT GTT GAC CTA TCC ACT GCC ACA TGT GAA AAA CTA AAT TTG CAA ACT	345
Pro Val Asp Leu Ser Thr Ala Thr Cys Glu Lys Leu Asn Leu Gln Thr	
55 60 65 70	
TCA ACA AGC ATT CCA AAT GTT ACT GAG ATG AAA ACC AAC ATG AGC CTC	393
Ser Thr Ser Ile Pro Asn Val Thr Glu Met Lys Thr Asn Met Ser Leu	
75 80 85	
GGC TTG ATC CTC ACC AGG AAC ATG GGA ACT GGA GGT TTT CTC ACA TGT	441
Gly Leu Ile Leu Thr Arg Asn Met Gly Thr Gly Gly Phe Leu Thr Cys	
90 95 100	
GGT CCT CTG TGG GCA CAG CAA TGT GGG AAT CAG TAT TAC ACA ACG GGT	489
Gly Pro Leu Trp Ala Gln Gln Cys Gly Asn Gln Tyr Tyr Thr Thr Gly	
105 110 115	
GTG TGT TCT GAC ATC AGT CCT GAT TTT CAG CTC TCA GCC AGC TTC TCA	537
Val Cys Ser Asp Ile Ser Pro Asp Phe Gln Leu Ser Ala Ser Phe Ser	
120 125 130	
CCT GCA ACT CAG CCC TGC CCT TCC CTC ATA GAT GTT GTG GTT GTG TGT	585
Pro Ala Thr Gln Pro Cys Pro Ser Leu Ile Asp Val Val Val Val Cys	
135 140 145 150	
GAT GAA TCA AAT AGT ATT TAT CCT TGG GAT GCA GTA AAG AAT TTT TTG	633
Asp Glu Ser Asn Ser Ile Tyr Pro Trp Asp Ala Val Lys Asn Phe Leu	
155 160 165	
GAA AAA TTT GTA CAA GGC CTT GAT ATA GGC CCC ACA AAG ACA CAG GTG	681
Glu Lys Phe Val Gln Gly Leu Asp Ile Gly Pro Thr Lys Thr Gln Val	
170 175 180	
GGG TTA ATT CAG TAT GCC AAT AAT CCA AGA GTT GTG TTT AAC TTG AAC	729
Gly Leu Ile Gln Tyr Ala Asn Asn Pro Arg Val Val Phe Asn Leu Asn	
185 190 195	
ACA TAT AAA ACC AAA GAA GAA ATG ATT GTA GCA ACA TCC CAG ACA TCC	777
Thr Tyr Lys Thr Lys Glu Glu Met Ile Val Ala Thr Ser Gln Thr Ser	
200 205 210	
CAA TAT GGT GGG GAC CTC ACA AAC ACA TTC GGA GCA ATT CAA TAT GCA	825
Gln Tyr Gly Gly Asp Leu Thr Asn Thr Phe Gly Ala Ile Gln Tyr Ala	
215 220 225 230	
AGA AAA TAT GCC TAT TCA GCA GCT TCT GGT GGG CGA CGA AGT GCT ACG	873
Arg Lys Tyr Ala Tyr Ser Ala Ala Ser Gly Gly Arg Arg Ser Ala Thr	
235 240 245	
AAA GTA ATG GTA GTT GTA ACT GAC GGT GAA TCA CAT GAT GGT TCA ATG	921
Lys Val Met Val Val Val Thr Asp Gly Glu Ser His Asp Gly Ser Met	
250 255 260	

TTG AAA GCT GTG ATT GAT CAA TGC AAC CAT GAC AAT ATA CTG AGG TTT	969
Leu Lys Ala Val Ile Asp Gln Cys Asn His Asp Asn Ile Leu Arg Phe	
265 270 275	
GGC ATA GCA GTT CTT GGG TAC TTA AAC AGA AAC GCC CTT GAT ACT AAA	1017
Gly Ile Ala Val Leu Gly Tyr Leu Asn Arg Asn Ala Leu Asp Thr Lys	
280 285 290	
AAT TTA ATA AAA GAA ATA AAA GCG ATC GCT AGT ATT CCA ACA GAA AGA	1065
Asn Leu Ile Lys Glu Ile Lys Ala Ile Ala Ser Ile Pro Thr Glu Arg	
295 300 305 310	
TAC TTT TTC AAT GTG TCT GAT GAA GCA GCT CTA CTA GAA AAG GCT GGG	1113
Tyr Phe Phe Asn Val Ser Asp Glu Ala Ala Leu Leu Glu Lys Ala Gly	
315 320 325	
ACA TTA GGA GAA CAA ATT TTC AGC ATT GAA GGT ACT GTT CAA GGA GGA	1161
Thr Leu Gly Glu Gln Ile Phe Ser Ile Glu Gly Thr Val Gln Gly Gly	
330 335 340	
GAC AAC TTT CAG ATG GAA ATG TCA CAA GTG GGA TTC AGT GCA GAT TAC	1209
Asp Asn Phe Gln Met Glu Met Ser Gln Val Gly Phe Ser Ala Asp Tyr	
345 350 355	
TCT TCT CAA AAT GAT ATT CTG ATG CTG GGT GCA GTG GGA GCT TTT GGC	1257
Ser Ser Gln Asn Asp Ile Leu Met Leu Gly Ala Val Gly Ala Phe Gly	
360 365 370	
TGG AGT GGG ACC ATT GTC CAG AAG ACA TCT CAT GGC CAT TTG ATC TTT	1305
Trp Ser Gly Thr Ile Val Gln Lys Thr Ser His Gly His Leu Ile Phe	
375 380 385 390	
CCT AAA CAA GCC TTT GAC CAA ATT CTG CAG GAC AGA AAT CAC AGT TCA	1353
Pro Lys Gln Ala Phe Asp Gln Ile Leu Gln Asp Arg Asn His Ser Ser	
395 400 405	
TAT TTA GGT TAC TCT GTG GCT GCA ATT TCT ACT GGA GAA AGC ACT CAC	1401
Tyr Leu Gly Tyr Ser Val Ala Ala Ile Ser Thr Gly Glu Ser Thr His	
410 415 420	
TTT GTT GCT GGT GCT CCT CGG GCA AAT TAT ACC GGC CAG ATA GTG CTA	1449
Phe Val Ala Gly Ala Pro Arg Ala Asn Tyr Thr Gly Gln Ile Val Leu	
425 430 435	
TAT AGT GTG AAT GAG AAT GGC AAT ATC ACG GTT ATT CAG GCT CAC CGA	1497
Tyr Ser Val Asn Glu Asn Gly Asn Ile Thr Val Ile Gln Ala His Arg	
440 445 450	
GGT GAC CAG ATT GGC TCC TAT TTT GGT AGT GTG CTG TGT TCA GTT GAT	1545
Gly Asp Gln Ile Gly Ser Tyr Phe Gly Ser Val Leu Cys Ser Val Asp	
455 460 465 470	
GTG GAT AAA GAC ACC ATT ACA GAC GTG CTC TTG GTA GGT GCA CCA ATG	1593
Val Asp Lys Asp Thr Ile Thr Asp Val Leu Leu Val Gly Ala Pro Met	
475 480 485	

TAC	ATG	AGT	GAC	CTA	AAG	AAA	GAG	GAA	GGA	AGA	GTC	TAC	CTG	TTT	ACT	1641
Tyr	Met	Ser	Asp	Leu	Lys	Lys	Glu	Glu	Gly	Arg	Val	Tyr	Leu	Phe	Thr	
			490					495					500			
ATC	AAA	AAG	GGC	ATT	TTG	GGT	CAG	CAC	CAA	TTT	CTT	GAA	GGC	CCC	GAG	1689
Ile	Lys	Lys	Gly	Ile	Leu	Gly	Gln	His	Gln	Phe	Leu	Glu	Gly	Pro	Glu	
		505					510					515				
GGC	ATT	GAA	AAC	ACT	CGA	TTT	GGT	TCA	GCA	ATT	GCA	GCT	CTT	TCA	GAC	1737
Gly	Ile	Glu	Asn	Thr	Arg	Phe	Gly	Ser	Ala	Ile	Ala	Ala	Leu	Ser	Asp	
	520					525					530					
ATC	AAC	ATG	GAT	GGC	TTT	AAT	GAT	GTG	ATT	GTT	GGT	TCA	CCA	CTA	GAA	1785
Ile	Asn	Met	Asp	Gly	Phe	Asn	Asp	Val	Ile	Val	Gly	Ser	Pro	Leu	Glu	
535					540				545						550	
AAT	CAG	AAT	TCT	GGA	GCT	GTA	TAC	ATT	TAC	AAT	GGT	CAT	CAG	GGC	ACT	1833
Asn	Gln	Asn	Ser	Gly	Ala	Val	Tyr	Ile	Tyr	Asn	Gly	His	Gln	Gly	Thr	
			555					560						565		
ATC	CGC	ACA	AAG	TAT	TCC	CAG	AAA	ATC	TTG	GGA	TCC	GAT	GGA	GCC	TTT	1881
Ile	Arg	Thr	Lys	Tyr	Ser	Gln	Lys	Ile	Leu	Gly	Ser	Asp	Gly	Ala	Phe	
			570					576					580			
AGG	AGC	CAT	CTC	CAG	TAC	TTT	GGG	AGG	TCC	TTG	GAT	GGC	TAT	GGA	GAT	1929
Arg	Ser	His	Leu	Gln	Tyr	Phe	Gly	Arg	Ser	Leu	Asp	Gly	Tyr	Gly	Asp	
		585					590					595				
TTA	AAT	GGG	GAT	TCC	ATC	ACC	GAT	GTG	TCT	ATT	GGT	GCC	TTT	GGA	CAA	1977
Leu	Asn	Gly	Asp	Ser	Ile	Thr	Asp	Val	Ser	Ile	Gly	Ala	Phe	Gly	Gln	
	600					605					610					
GTG	GTT	CAA	CTC	TGG	TCA	CAA	AGT	ATT	GCT	GAT	GTA	GCT	ATA	GAA	GCT	2025
Val	Val	Gln	Leu	Trp	Ser	Gln	Ser	Ile	Ala	Asp	Val	Ala	Ile	Glu	Ala	
615					620				625						630	
TCA	TTC	ACA	CCA	GAA	AAA	ATC	ACT	TTG	GTC	AAC	AAG	AAT	GCT	CAG	ATA	2073
Ser	Phe	Thr	Pro	Glu	Lys	Ile	Thr	Leu	Val	Asn	Lys	Asn	Ala	Gln	Ile	
			635					640						645		
ATT	CTC	AAA	CTC	TGC	TTC	AGT	GCA	AAG	TTC	AGA	CCT	ACT	AAG	CAA	AAC	2121
Ile	Leu	Lys	Leu	Cys	Phe	Ser	Ala	Lys	Phe	Arg	Pro	Thr	Lys	Gln	Asn	
			650					655					660			
AAT	CAA	GTG	GCC	ATT	GTA	TAT	AAC	ATC	ACA	CTT	GAT	GCA	GAT	GGA	TTT	2169
Asn	Gln	Val	Ala	Ile	Val	Tyr	Asn	Ile	Thr	Leu	Asp	Ala	Asp	Gly	Phe	
		665					670					675				
TCA	TCC	AGA	GTA	ACC	TCC	AGG	GGG	TTA	TTT	AAA	GAA	AAC	AAT	GAA	AGG	2217
Ser	Ser	Arg	Val	Thr	Ser	Arg	Gly	Leu	Phe	Lys	Glu	Asn	Asn	Glu	Arg	
		680				685					690					
TGC	CTG	CAG	AAG	AAT	ATG	GTA	GTA	AAT	CAA	GCA	CAG	AGT	TGC	CCC	GAG	2265

CAC	ATC	ATT	TAT	ATA	CAG	GAG	CCC	TCT	GAT	GTT	GTC	AAC	TCT	TTG	GAT	2313
His	Ile	Ile	Tyr	Ile	Gln	Glu	Pro	Ser	Asp	Val	Val	Asn	Ser	Leu	Asp	
				725					730						735	
TTG	CGT	GTG	GAC	ATC	AGT	CTG	GAA	AAC	CCT	GGC	ACT	AGC	CCT	GCC	CTT	2361
Leu	Arg	Val	Asp	Ile	Ser	Leu	Glu	Asn	Pro	Gly	Thr	Ser	Pro	Ala	Leu	
			740					745					750			
GAA	GCC	TAT	TCT	GAG	ACT	GCC	AAG	GTC	TTC	AGT	ATT	CCT	TTC	CAC	AAA	2409
Glu	Ala	Tyr	Ser	Glu	Thr	Ala	Lys	Val	Phe	Ser	Ile	Pro	Phe	His	Lys	
		755					760					765				
GAC	TGT	GGT	GAG	GAT	GGA	CTT	TGC	ATT	TCT	GAT	CTA	GTC	CTA	GAT	GTC	2457
Asp	Cys	Gly	Glu	Asp	Gly	Leu	Cys	Ile	Ser	Asp	Leu	Val	Leu	Asp	Val	
	760					765					770					
CGA	CAA	ATA	CCA	GCT	GCT	CAA	GAA	CAA	CCC	TTT	ATT	GTC	AGC	AAC	CAA	2505
Arg	Gln	Ile	Pro	Ala	Ala	Gln	Glu	Gln	Pro	Phe	Ile	Val	Ser	Asn	Gln	
	775				780					785					790	
AAC	AAA	AGG	TTA	ACA	TTT	TCA	GTA	ACA	CTG	AAA	AAT	AAA	AGG	GAA	AGT	2553
Asn	Lys	Arg	Leu	Thr	Phe	Ser	Val	Thr	Leu	Lys	Asn	Lys	Arg	Glu	Ser	
			795						800					805		
GCA	TAC	AAC	ACT	GGA	ATT	GTT	GTT	GAT	TTT	TCA	GAA	AAC	TTG	TTT	TTT	2601
Ala	Tyr	Asn	Thr	Gly	Ile	Val	Val	Asp	Phe	Ser	Glu	Asn	Leu	Phe	Phe	
			810					815					820			
GCA	TCA	TTC	TCC	CTA	CCG	GTT	GAT	GGG	ACA	GAA	GTA	ACA	TGC	CAG	GTG	2649
Ala	Ser	Phe	Ser	Leu	Pro	Val	Asp	Gly	Thr	Glu	Val	Thr	Cys	Gln	Val	
		825					830					835				
GCT	GCA	TCT	CAG	AAG	TCT	GTT	GCC	TGC	GAT	GTA	GGC	TAC	CCT	GCT	TTA	2697
Ala	Ala	Ser	Gln	Lys	Ser	Val	Ala	Cys	Asp	Val	Gly	Tyr	Pro	Ala	Leu	
	840					845					850					
AAG	AGA	GAA	CAA	CAG	GTG	ACT	TTT	ACT	ATT	AAC	TTT	GAC	TTC	AAT	CTT	2745
Lys	Arg	Glu	Gln	Gln	Val	Thr	Phe	Thr	Ile	Asn	Phe	Asp	Phe	Asn	Leu	
	855				860					865					870	
CAA	AAC	CTT	CAG	AAT	CAG	GCG	TCT	CTC	AGT	TTC	CAA	GCC	TTA	AGT	GAA	2793
Gln	Asn	Leu	Gln	Asn	Gln	Ala	Ser	Leu	Ser	Phe	Gln	Ala	Leu	Ser	Glu	
			875					880						885		
AGC	CAA	GAA	GAA	AAC	AAG	GCT	GAT	AAT	TTG	GTC	AAC	CTC	AAA	ATT	CCT	2841
Ser	Gln	Glu	Glu	Asn	Lys	Ala	Asp	Asn	Leu	Val	Asn	Leu	Lys	Ile	Pro	
			890					895					900			
CTC	CTG	TAT	GAT	GCT	GAA	ATT	CAC	TTA	ACA	AGA	TCT	ACC	AAC	ATA	AAT	2889
Leu	Leu	Tyr	Asp	Ala	Glu	Ile	His	Leu	Thr	Arg	Ser	Thr	Asn	Ile	Asn	
		905					910					915				
TTT	TAT	GAA	ATC	TCT	TCG	GAT	GGG	AAT	GTT	CCT	TCA	ATC	GTG	CAC	AGT	2937
Phe	Tyr	Glu	Ile	Ser	Ser	Asp	Gly	Asn	Val	Pro	Ser	Ile	Val	His	Ser	
	920					925					930					

[illegible]

GGGAACCGGC AGCATCCCAG CCAGGGTTTG CTGTTTGCCT GCATGGATTT CTTTTTAAAT 3675
 CCCATATTTT TTTTATCATG TCGTAGGTAA ACTAACCTGG TATTTTAAGA GAAACTGCA 3735
 GGTCAGTTTG GATGAAGAAA TTGTGGGGGG TGGGGGAGGT GCGGGGGGCA GGTAGGGAAA 3795
 TAATAGGGAA AATACCTATT TTATATGATG GGGGAAAAAA AGTAATCTTT AAAGTGGCTG 3855
 GCCCAGAGTT TACATTCTAA TTTGCATTGT GTCAGAAACA TGAAATGCTT CCAAGCATGA 3915
 CAACTTTTAA AGAAAAATAT GATACTCTCA GATTTTAAGG GGGAAAACTG TTCTCTTTAA 3975
 AATATTTGTC TTTAAACAGC AACTACAGAA GTGGAAGTGC TTGATATGTA AGTACTTCCA 4035
 CTTGTGTATA TTTAATGAA TATTGATGTT AACAAGAGGG GAAAACAAAA CACAGGTTTT 4095
 TTCAATTTAT GCTGCTCATC CAAAGTTGCC ACAGATGATA CTTCCAAGTG ATAATTTTAT 4155
 TTATAAACTA GGTAAATTT GTTGTGGTT CTTTTTATAC CACGGCTGCC CTTCCACAC 4215
 CCCATCTTGC TCTAATGATC AAAACATGCT TGAATAACTG AGCTTAGAGT ATACCTCCTA 4275
 TATGTCCATT TAAGTTAGGA GAGGGGGCGA TATAGAGACT AAGGCACAAA ATTTTGTTTTA 4335
 AAATCAGAA TATAACATTT ATGTAAATC CCATCTGCTA GAAGCCCATC CTGTGCCAGA 4395
 GGAAGGAAAA GGAGGAAATT TCCTTTCTCT TTTAGGAGGC ACAACAGTTC TCTTCTAGGA 4455
 TTTGTTTGGC TGACTGGCAG TAACCTAGTG AATTTTGAAG AGATGAGTAA TTTCTTTGGC 4515
 AACCTTCTC CTCCCTTACT GAACCACTCT CCCACCTCCT GGTGGTACCA TTATTATAGA 4575
 AGCCCTCTAC AGCCTGACTT TCTCTCCAGC GGTCCAAAGT TATCCCCTCC TTTACCCCTC 4635
 ATCCAAAGTT CCCACTCCTT CAGGACAGCT GCTGTGCATT AGATATTAGG GGGGAAAGTC 4695
 ATCTGTTTAA TTTACACACT TGCATGAATT ACTGTATATA AACTCCTTAA CTTCAGGGAG 4755
 CTATTTTCAT TTAGTGCTAA ACAAGTAAGA AAAATAAGCT AGAGTGAATT TCTAAATGTT 4815
 GGAATGTTAT GGGATGTAAA CAATGTAAAG TAAACACTC TCAGGATTTT ACCAGAAGTT 4875
 ACAGATGAGG CACTGGAAAC CACCACCAA TTAGCAGGTG CACCTTCTGT GGCTGTCTTG 4935
 TTTCTGAAGT ACTTTTCTT CCACAAGAGT GAATTTGACC TAGGCAAGTT TGTTCAAAAG 4995
 GTAGATCCTG AGATGATTTG GTCAGATTGG GATAAGGCC AGCAATCTGC ATTTTAACAA 5055
 GCACCCAGT CACTAGGATG CAGATGGACC ACACCTTGAG AAACACCACC CATTTCTACT 5115
 TTTTGCACCT TATTTTCTCT GTTCCTGAGC CCCACATTC TCTAGGAGAA ACTTAGATTA 5175
 AAATTCACAG ACACTACATA TCTAAAGCTT TGACAAGTCC TTGACCTCTA TAACTTCAG 5235
 AGTCCTCATT ATAAAATGGG AAGACTGAGC TGGAGTTCAG CAGTGATGCT TTTTAGTTTT 5295
 AAAAGTCTAT GATCTGATCT GGACTTCCTA TAATACAAAT ACACAATCCT CCAAGAATTT 5355
 GACTTGAAAA AGGAATTC 5373

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Gly Pro Glu Arg Thr Gly Ala Ala Pro Leu Pro Leu Leu Val
 -29 -25 -20 -15

Leu Ala Leu Ser Gln Gly Ile Leu Asn Cys Cys Leu Ala Tyr Asn Val
 -10 -5 1

Gly Leu Pro Glu Ala Lys Ile Phe Ser Gly Pro Ser Ser Glu Gln Phe
 5 10 15

Gly	Tyr	Ala	Val	Gln	Gln	Phe	Ile	Asn	Pro	Lys	Gly	Asn	Trp	Leu	Leu
20					25					30					35
Val	Gly	Ser	Pro	Trp	Ser	Gly	Phe	Pro	Glu	Asn	Arg	Met	Gly	Asp	Val
				40					45					50	
Tyr	Lys	Cys	Pro	Val	Asp	Leu	Ser	Thr	Ala	Thr	Cys	Glu	Lys	Leu	Asn
			55					60					65		
Leu	Gln	Thr	Ser	Thr	Ser	Ile	Pro	Asn	Val	Thr	Glu	Met	Lys	Thr	Asn
		70					75					80			
Met	Ser	Leu	Gly	Leu	Ile	Leu	Thr	Arg	Asn	Met	Gly	Thr	Gly	Gly	Phe
	85					90					95				
Leu	Thr	Cys	Gly	Pro	Leu	Trp	Ala	Gln	Gln	Cys	Gly	Asn	Gln	Tyr	Tyr
100					105				110						115
Thr	Thr	Gly	Val	Cys	Ser	Asp	Ile	Ser	Pro	Asp	Phe	Gln	Leu	Ser	Ala
				120					125					130	
Ser	Phe	Ser	Pro	Ala	Thr	Gln	Pro	Cys	Pro	Ser	Leu	Ile	Asp	Val	Val
			135					140					145		
Val	Val	Cys	Asp	Glu	Ser	Asn	Ser	Ile	Tyr	Pro	Trp	Asp	Ala	Val	Lys
		150					155					160			
Asn	Phe	Leu	Glu	Lys	Phe	Val	Gln	Gly	Leu	Asp	Ile	Gly	Pro	Thr	Lys
	165					170					175				
Thr	Gln	Val	Gly	Leu	Ile	Gln	Tyr	Ala	Asn	Asn	Pro	Arg	Val	Val	Phe
180					185					190					195
Asn	Leu	Asn	Thr	Tyr	Lys	Thr	Lys	Glu	Glu	Met	Ile	Val	Ala	Thr	Ser
				200					205					210	
Gln	Thr	Ser	Gln	Tyr	Gly	Gly	Asp	Leu	Thr	Asn	Thr	Phe	Gly	Ala	Ile
			215					220					225		
Gln	Tyr	Ala	Arg	Lys	Tyr	Ala	Tyr	Ser	Ala	Ala	Ser	Gly	Gly	Arg	Arg
		230					235					240			
Ser	Ala	Thr	Lys	Val	Met	Val	Val	Val	Thr	Asp	Gly	Glu	Ser	His	Asp
	245					250					255				
Gly	Ser	Met	Leu	Lys	Ala	Val	Ile	Asp	Gln	Cys	Asn	His	Asp	Asn	Ile
260					265					270					275
Leu	Arg	Phe	Gly	Ile	Ala	Val	Leu	Gly	Tyr	Leu	Asn	Arg	Asn	Ala	Leu
				280					285					290	
Asp	Thr	Lys	Asn	Leu	Ile	Lys	Glu	Ile	Lys	Ala	Ile	Ala	Ser	Ile	Pro
			295					300					305		
Thr	Glu	Arg	Tyr	Phe	Phe	Asn	Val	Ser	Asp	Glu	Ala	Ala	Leu	Leu	Glu
		310					315					320			

Lys Ala Gly Thr Leu Gly Glu Gln Ile Phe Ser Ile Glu Gly Thr Val
 325 330 335
 Gln Gly Gly Asp Asn Phe Gln Met Glu Met Ser Gln Val Gly Phe Ser
 340 345 350 355
 Ala Asp Tyr Ser Ser Gln Asn Asp Ile Leu Met Leu Gly Ala Val Gly
 360 365 370
 Ala Phe Gly Trp Ser Gly Thr Ile Val Gln Lys Thr Ser His Gly His
 375 380 385
 Leu Ile Phe Pro Lys Gln Ala Phe Asp Gln Ile Leu Gln Asp Arg Asn
 390 395 400
 His Ser Ser Tyr Leu Gly Tyr Ser Val Ala Ala Ile Ser Thr Gly Glu
 405 410 415
 Ser Thr His Phe Val Ala Gly Ala Pro Arg Ala Asn Tyr Thr Gly Gln
 420 425 430 435
 Ile Val Leu Tyr Ser Val Asn Glu Asn Gly Asn Ile Thr Val Ile Gln
 440 445 450
 Ala His Arg Gly Asp Gln Ile Gly Ser Tyr Phe Gly Ser Val Leu Cys
 455 460 465
 Ser Val Asp Val Asp Lys Asp Thr Ile Thr Asp Val Leu Leu Val Gly
 470 475 480
 Ala Pro Met Tyr Met Ser Asp Leu Lys Lys Glu Glu Gly Arg Val Tyr
 485 490 495
 Leu Phe Thr Ile Lys Lys Gly Ile Leu Gly Gln His Gln Phe Leu Glu
 500 505 510 515
 Gly Pro Glu Gly Ile Glu Asn Thr Arg Phe Gly Ser Ala Ile Ala Ala
 520 525 530
 Leu Ser Asp Ile Asn Met Asp Gly Phe Asn Asp Val Ile Val Gly Ser
 535 540 545
 Pro Leu Glu Asn Gln Asn Ser Gly Ala Val Tyr Ile Tyr Asn Gly His
 550 555 560
 Gln Gly Thr Ile Arg Thr Lys Tyr Ser Gln Lys Ile Leu Gly Ser Asp
 565 570 575
 Gly Ala Phe Arg Ser His Leu Gln Tyr Phe Gly Arg Ser Leu Asp Gly
 580 585 590 595
 Tyr Gly Asp Leu Asn Gly Asp Ser Ile Thr Asp Val Ser Ile Gly Ala
 600 605 610
 Phe Gly Gln Val Val Gln Leu Trp Ser Gln Ser Ile Ala Asp Val Ala
 615 620 625

Ile Glu Ala Ser Phe Thr Pro Glu Lys Ile Thr Leu Val Asn Lys Asn
 630 635 640
 Ala Gln Ile Ile Leu Lys Leu Cys Phe Ser Ala Lys Phe Arg Pro Thr
 645 650 655
 Lys Gln Asn Asn Gln Val Ala Ile Val Tyr Asn Ile Thr Leu Asp Ala
 660 665 670 675
 Asp Gly Phe Ser Ser Arg Val Thr Ser Arg Gly Leu Phe Lys Glu Asn
 680 685 690
 Asn Glu Arg Cys Leu Gln Lys Asn Met Val Val Asn Gln Ala Gln Ser
 695 700 705
 Cys Pro Glu His Ile Ile Tyr Ile Gln Glu Pro Ser Asp Val Val Asn
 710 715 720
 Ser Leu Asp Leu Arg Val Asp Ile Ser Leu Glu Asn Pro Gly Thr Ser
 725 730 735
 Pro Ala Leu Glu Ala Tyr Ser Glu Thr Ala Lys Val Phe Ser Ile Pro
 740 745 750 755
 Phe His Lys Asp Cys Gly Glu Asp Gly Leu Cys Ile Ser Asp Leu Val
 760 765 770
 Leu Asp Val Arg Gln Ile Pro Ala Ala Gln Glu Gln Pro Phe Ile Val
 775 780 785
 Ser Asn Gln Asn Lys Arg Leu Thr Phe Ser Val Thr Leu Lys Asn Lys
 790 795 800
 Arg Glu Ser Ala Tyr Asn Thr Gly Ile Val Val Asp Phe Ser Glu Asn
 805 810 815
 Leu Phe Phe Ala Ser Phe Ser Leu Pro Val Asp Gly Thr Glu Val Thr
 820 825 830 835
 Cys Gln Val Ala Ala Ser Gln Lys Ser Val Ala Cys Asp Val Gly Tyr
 840 845 850
 Pro Ala Leu Lys Arg Glu Gln Gln Val Thr Phe Thr Ile Asn Phe Asp
 855 860 865
 Phe Asn Leu Gln Asn Leu Gln Asn Gln Ala Ser Leu Ser Phe Gln Ala
 870 875 880
 Leu Ser Glu Ser Gln Glu Glu Asn Lys Ala Asp Asn Leu Val Asn Leu
 885 890 895
 Lys Ile Pro Leu Leu Tyr Asp Ala Glu Ile His Leu Thr Arg Ser Thr
 900 905 910 915
 Asn Ile Asn Phe Tyr Glu Ile Ser Ser Asp Gly Asn Val Pro Ser Ile
 920 925 930

Asn Pro Asp Glu Ile Asp Glu Thr Thr Glu Leu Ser Ser
1140 1145 1150

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCAGAGTCAC TCTCACAGAG

20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CACAGCGTAC ACGTACACC

19

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CACTTATAGA CATCTCCAG

19

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- ```
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CATCCATGTT GATGTCTG

18

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- ```
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CATGTGATTC ACCGTCAG

18

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- ```
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCATATTGAA TTGCTCCGAA TGTG

24

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCGTATGCA CAACGCA

17

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCGACAGCTG ACCAGTCAGC A

21

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CACTCCTCCA CAGCTCCT

18

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ACATGTACTC ACTGG

15

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTCACATGTG GTCCTCTG

18

## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTCCTGTTGA CCTATCCACT GC

22

## WE CLAIM:

1. A method to identify a mammal having or at risk for developing glomerulopathy comprising the steps of:

5 analyzing a tissue sample from a mammal known to contain cells expressing integrin RNA or protein for integrin subunit expression; and  
comparing integrin subunit expression in the sample with a control tissue sample, wherein altered integrin subunit expression is correlated with glomerulopathy.

10 2. The method of Claim 1, wherein the mammal is a human.

3. The method of Claim 1, wherein the tissue sample is a kidney biopsy.

4. The method of Claim 1, wherein the tissue sample is blood.

15 5. The method of Claim 4, wherein the blood sample contains polymorphonuclear cells or monocytes.

6. The method of Claim 1, wherein the tissue sample is a skin biopsy.

20 7. The method of Claim 1, wherein said analysis comprises *in situ* hybridization.

8. The method of Claim 7, wherein said *in situ* hybridization comprises PCR enhanced *in situ* hybridization.

25 9. The method of Claim 1, wherein said analyzing comprises isolating RNA from the sample.

30 10. The method of Claim 1, wherein said analyzing comprises performing PCR, detecting amplified fragments from an integrin subunit and comparing the amount of amplified fragments to the amount of amplified fragments obtained from the control.

11. The method of claim 1, wherein the integrin subunit is an alpha integrin subunit.

12. The method of Claim 11, wherein the  $\alpha$  integrin subunit is  $\alpha 1$ ,  $\alpha 2$ ,  $\alpha 3$ , or  $\alpha 5$  integrin subunit.

13. The method of claim 12, wherein the  $\alpha$  integrin subunit is  $\alpha 1$  or  $\alpha 2$  integrin subunit.

14. The method of claim 1, wherein a decrease in  $\alpha 1$  integrin subunit in the tissue sample as compared with control tissue is correlated with nephropathy.

15. The method of claim 1, wherein an increase in  $\alpha 2$ ,  $\alpha 3$ ,  $\alpha 5$ , or  $\beta 1$  integrin subunit in the tissue sample as compared with control tissue is correlated with nephropathy.

16. The method of claim 1, wherein an increase in  $\alpha 2$  and a decrease in  $\alpha 1$  integrin subunit in the tissue sample as compared with control tissue is correlated with nephropathy.

17. The method of Claim 7, wherein a nucleic acid probe is used to detect integrin, and the probe comprises a 3.9kb fragment of  $\alpha 1$  from the 5' end to nucleotide 3900.

18. The method of Claim 7, wherein a nucleic acid probe is used to detect integrin, and the probe comprises a 1.8kb fragment of  $\alpha 2$  from 5' end through the EcoRI site at nucleotide 1800.

19. The method of Claim 1, wherein said analyzing comprises incubating the sample with an anti-integrin subunit antibody.

20. The method of Claim 1, wherein the nondiabetic control sample is from a mammal with no history of hypertension.

21. The method of Claim 1, wherein an increase of about 25% - 100% in the level of  $\alpha 2$  integrin subunit expression in the sample tissue as compared with the control is correlated with nephropathy.

5 22. The method of Claim 1, wherein a decrease of about 25% - 100% in the level of  $\alpha 1$  integrin subunit expression in the sample tissue as compared with the control is correlated with nephropathy.

10 23. A method to identify a mammal having or at risk for developing glomerulopathy comprising the steps of:

analyzing a tissue sample from a mammal known to contain cells expressing integrin protein for  $\alpha 1$  and  $\alpha 2$  integrin subunit expression as compared with a control tissue sample; and

15 correlating a decreased level of  $\alpha 1$  integrin subunit expression and/or an increased level of  $\alpha 2$  integrin subunit expression in the sample tissue as compared to the control with nephropathy.

20 24. A method to identify a mammal with diabetes who has or is at risk for developing secondary pathological changes associated with diabetes comprising the steps of:

analyzing a tissue sample from a mammal known to contain cells expressing integrin protein for integrin subunit expression; and

25 correlating alterations in the level of expression of least one integrin subunit as compared with a control tissue sample with the presence of or the risk for developing secondary pathological changes associated with diabetes.

25. The method of claim 25, wherein said integrin subunit is  $\alpha 1$ ,  $\alpha 2$ ,  $\alpha 3$ ,  $\alpha 5$ , or  $\beta 1$ .

30 26. The method of claim 25, wherein said integrin subunit is  $\alpha 1$  or  $\alpha 2$ .

27. The method of claim 1, wherein said comparing of a sample with a control comprises comparing a first sample obtained from an individual with a second sample obtained from the same individual at a later sampling time.

5 28. A kit for the diagnosis of nephropathy comprising:  
two sets of hybridization probes or antibodies capable of detecting each of  $\alpha 1$   
and  $\alpha 2$  integrin subunit expression in a tissue sample.

10 29. The kit of claim 28 further comprising primer sets for the amplification of  $\alpha 1$   
and  $\alpha 2$  integrin subunits.

30. The kit of claim 28 further comprising control, standard  $\alpha 1$  and  $\alpha 2$  integrin subunits.

PCT

INTELLECTUAL PROPERTY ORGANIZATION  
International Bureau



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

|                                                                                                                                                                                                                                                                                                                                                                                                     |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |                                                                           |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------|
| <b>(51) International Patent Classification <sup>6</sup> :</b><br><b>C12Q 1/68, C07K 14/705, 16/28, G01N 33/566</b>                                                                                                                                                                                                                                                                                 |  | <b>A1</b>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | <b>(11) International Publication Number:</b><br><b>WO 97/04133</b>       |
|                                                                                                                                                                                                                                                                                                                                                                                                     |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | <b>(43) International Publication Date:</b><br>6 February 1997 (06.02.97) |
| <b>(21) International Application Number:</b><br>PCT/US96/12067                                                                                                                                                                                                                                                                                                                                     |  | <b>(81) Designated States:</b> AL, AM, AT, AT (Utility model), AU, AZ, BB, BG, BR, BY, CA, CH, CN, CU, CZ, CZ (Utility model), DE, DE (Utility model), DK, DK (Utility model), EE, EE (Utility model), ES, FI, FI (Utility model), GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SK (Utility model), TJ, TM, TR, TT, UA, UG, US, UZ, VN, ARIPO patent (KE, LS, MW, SD, SZ, UG), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). |                                                                           |
| <b>(22) International Filing Date:</b><br>19 July 1996 (19.07.96)                                                                                                                                                                                                                                                                                                                                   |  | <b>Published</b><br><i>With international search report.</i><br><i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |                                                                           |
| <b>(30) Priority Data:</b><br>60/001,387 21 July 1995 (21.07.95) US<br>60/001,861 3 August 1995 (03.08.95) US<br>60/016,700 2 May 1996 (02.05.96) US                                                                                                                                                                                                                                                |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |                                                                           |
| <b>(71) Applicant (for all designated States except US):</b> REGENTS OF THE UNIVERSITY OF MINNESOTA [US/US]; Morrill Hall, 100 Church Street, S.E., Minneapolis, MN 55455 (US).                                                                                                                                                                                                                     |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |                                                                           |
| <b>(72) Inventors; and</b>                                                                                                                                                                                                                                                                                                                                                                          |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |                                                                           |
| <b>(75) Inventors/Applicants (for US only):</b> TSILIBARY, Photini-Effie [US/US]; 1812 Emerson Avenue South, Minneapolis, MN 55403 (US). CHARONIS, Aristidis, S. [US/US]; 1812 Emerson Avenue South, Minneapolis, MN 55403 (US). SETTY, Suman [IN/US]; Apartment 1703, 425 15th Avenue S.E., Minneapolis, MN 55414 (US). MAUER, Michael [US/US]; 2507 West 52nd Street, Minneapolis, MN 55401 (US). |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |                                                                           |
| <b>(74) Agent:</b> BRUESS, Steven, C.; Merchant, Gould, Smith, Edell, Welter & Schmidt, 3100 Norwest Center, 90 South Seventh Street, Minneapolis, MN 55402 (US).                                                                                                                                                                                                                                   |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |                                                                           |
| <b>(54) Title:</b> ANALYSIS OF ALPHA INTEGRINS FOR THE DIAGNOSIS OF DIABETIC NEPHROPATHY                                                                                                                                                                                                                                                                                                            |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |                                                                           |
| <b>(57) Abstract</b><br><br>Analysis of alterations in integrin subunit expression, particularly $\alpha 1$ and/or $\alpha 2$ integrin subunit expression from integrin producing cells as compared to normal controls as a diagnostic method to identify individuals who have or are predisposed to pathologies associated with altered matrix deposition, such as diabetic renal nephropathy.     |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |                                                                           |



1/1

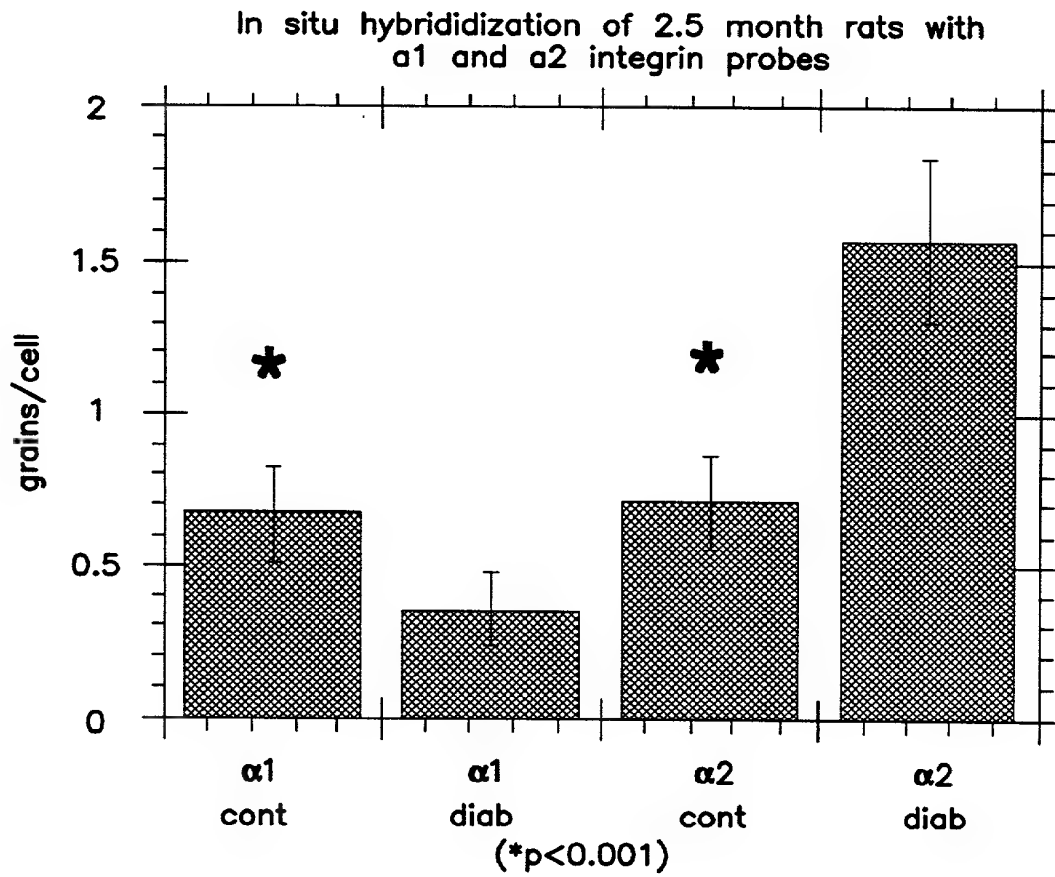


FIG. 1

S/N 09/000,004

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant: TSILIBARY, ET AL. Examiner: UNKNOWN  
Serial No.: 09/000,004 Group Art Unit: UNKNOWN  
Filed: JANUARY 21, 1998 Docket No.: 600.314USWO  
Title: ANALYSIS OF ALPHA INTEGRINS FOR THE DIAGNOSIS OF  
DIABETIC NEPHROPATHY

CERTIFICATE UNDER 37 CFR 1.8:

I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail, with sufficient postage, in an envelope addressed to. BOX PCT, Commissioner for Patents, Washington, D C 20231 on May 23, 2001.

*Anne Harrison*  
Anne Harrison

CHANGE OF ADDRESS

BOX PCT  
Commissioner for Patents  
Washington, D.C. 20231

Dear Sir:



Please change the correspondence address for the above-referenced patent application to:

Merchant & Gould P.C.  
P.O. Box 2903  
Minneapolis, Minnesota 55402-0903

If there are any questions regarding this matter, please call the undersigned at 612.332.5300.

Respectfully submitted,

MERCHANT & GOULD P.C.  
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Minneapolis, Minnesota 55402-0910  
(612) 332-5300

Date:

*May 23, 2001*

*Denise M. Kettelberger*  
Denise M. Kettelberger, Ph.D.  
Reg. No. 33,924  
DMK:KC:PSTalh

## United States Patent Application

## COMBINED DECLARATION AND POWER OF ATTORNEY

As a below named inventor I hereby declare that: my residence, post office address and citizenship are as stated below next to my name; that

I verily believe I am the original, first and sole inventor (if only one name is listed below) or a joint inventor (if plural inventors are named below) of the subject matter which is claimed and for which a patent is sought on the invention entitled: ANALYSIS OF ALPHA INTEGRINS FOR THE DIAGNOSIS OF DIABETIC NEPHROPATHY

The specification of which

- a. ☐ is attached hereto  
 b. ☒ was filed on January 21, 1998 as application serial no. and was amended on (if applicable) (in the case of a PCT-filed application) described and claimed in international no. PCT/US96/12067 filed 19 July 1996 and as amended on (if any), which I have reviewed and for which I solicit a United States patent.

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to the patentability of this application in accordance with Title 37, Code of Federal Regulations, § 1.56 (attached hereto).

I hereby claim foreign priority benefits under Title 35, United States Code, § 119/365 of any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on the basis of which priority is claimed:

- a. ☒ no such applications have been filed.  
 b. ☐ such applications have been filed as follows:

| FOREIGN APPLICATION(S), IF ANY, CLAIMING PRIORITY UNDER 35 USC § 119         |                    |                                      |                                     |
|------------------------------------------------------------------------------|--------------------|--------------------------------------|-------------------------------------|
| COUNTRY                                                                      | APPLICATION NUMBER | DATE OF FILING<br>(day, month, year) | DATE OF ISSUE<br>(day, month, year) |
|                                                                              |                    |                                      |                                     |
| ALL FOREIGN APPLICATION(S), IF ANY, FILED BEFORE THE PRIORITY APPLICATION(S) |                    |                                      |                                     |
| COUNTRY                                                                      | APPLICATION NUMBER | DATE OF FILING<br>(day, month, year) | DATE OF ISSUE<br>(day, month, year) |
|                                                                              |                    |                                      |                                     |

I hereby claim the benefit under Title 35, United States Code, § 120/365 of any United States and PCT international application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code, § 112, I acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, § 1.56(a) which occurred between the filing date of the prior application and the national or PCT international filing date of this application.

| U.S. APPLICATION NUMBER | DATE OF FILING (day, month, year) | STATUS (patented, pending, abandoned) |
|-------------------------|-----------------------------------|---------------------------------------|
|                         |                                   |                                       |

I hereby claim the benefit under Title 35, United States Code § 119(e) of any United States provisional application(s) listed below:

| U.S. PROVISIONAL APPLICATION NUMBER | DATE OF FILING (Day, Month, Year) |
|-------------------------------------|-----------------------------------|
| 60/001,387                          | July 21, 1995                     |
| 60/001,861                          | August 3, 1995                    |
| 60/016,700                          | May 2, 1996                       |

I hereby appoint the following attorney(s) and/or patent agent(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected herewith:

|                         |                          |                        |                           |
|-------------------------|--------------------------|------------------------|---------------------------|
| Albrecht, John W.       | Reg. No. <u>40,481</u>   | Lasky, Michael B.      | Reg. No. <u>29,555</u>    |
| Ansems, Gregory M.      | Reg. No. <u>P-42,264</u> | Lindquist, Timothy A.  | Reg. No. <u>40,701</u>    |
| Batzli, Brian H.        | Reg. No. <u>32,960</u>   | Lynch, David W.        | Reg. No. <u>36,204</u>    |
| Beard, John L.          | Reg. No. <u>27,612</u>   | Mau, Michael L.        | Reg. No. <u>30,087</u>    |
| Berman, Charles         | Reg. No. <u>29,249</u>   | Maunu, Leroy D.        | Reg. No. <u>35,274</u>    |
| Black, Bruce E.         | Reg. No. <u>P-41,622</u> | McDaniel, Karen D.     | Reg. No. <u>37,674</u>    |
| Bogucki, Raymond A.     | Reg. No. <u>17,426</u>   | McDonald, Daniel W.    | Reg. No. <u>32,044</u>    |
| Bruess, Steven C.       | Reg. No. <u>34,130</u>   | McIntyre, Iain A.      | Reg. No. <u>40,377</u>    |
| Byrne, Linda M.         | Reg. No. <u>32,404</u>   | Mueller, Douglas P.    | Reg. No. <u>30,300</u>    |
| Canady, Karen S.        | Reg. No. <u>39,927</u>   | Nasiedlak, Tyler L.    | Reg. No. <u>40,099</u>    |
| Carlson, Alan G.        | Reg. No. <u>25,959</u>   | Nelson, Albin J.       | Reg. No. <u>28,650</u>    |
| Carter, Charles G.      | Reg. No. <u>35,093</u>   | Orler, Anthony J.      | Reg. No. <u>41,232</u>    |
| Caspers, Philip P.      | Reg. No. <u>33,227</u>   | Pauly, Daniel M.       | Reg. No. <u>40,123</u>    |
| Chiapetta, James R.     | Reg. No. <u>39,634</u>   | Plunkett, Theodore     | Reg. No. <u>37,209</u>    |
| Clifford, John A.       | Reg. No. <u>30,247</u>   | Pytel, Melissa J.      | Reg. No. <u>P-41,512</u>  |
| Cooper, Victor G.       | Reg. No. <u>39,641</u>   | Reich, John C.         | Reg. No. <u>37,703</u>    |
| Crawford, Robert        | Reg. No. <u>32,122</u>   | Reiland, Earl D.       | Reg. No. <u>25,767</u>    |
| Daignault, Ronald A.    | Reg. No. <u>25,968</u>   | Rittmaster, Ted R.     | Reg. No. <u>32,933</u>    |
| Daley, Dennis R.        | Reg. No. <u>34,994</u>   | Schmaltz, David G.     | Reg. No. <u>39,828</u>    |
| Dalglish, Leslie E.     | Reg. No. <u>40,579</u>   | Schmidt, Cecil C.      | Reg. No. <u>20,566</u>    |
| Daulton, Julie R.       | Reg. No. <u>36,414</u>   | Schuman, Mark D.       | Reg. No. <u>31,197</u>    |
| DeVries Smith, Kate     | Reg. No. <u>P-42,157</u> | Schumann, Michael D.   | Reg. No. <u>30,422</u>    |
| DiPietro, Mark J.       | Reg. No. <u>28,707</u>   | Sebald, Gregory A.     | Reg. No. <u>33,280</u>    |
| Edell, Robert T.        | Reg. No. <u>20,187</u>   | Sharp, Janice A.       | Reg. No. <u>34,051</u>    |
| Epp Ryan, Sandra        | Reg. No. <u>39,667</u>   | Skoog, Mark T.         | Reg. No. <u>40,178</u>    |
| Farber, Michael B.      | Reg. No. <u>32,612</u>   | Smith, Jerome R.       | Reg. No. <u>35,684</u>    |
| Funk, Steven R.         | Reg. No. <u>37,830</u>   | Soderberg, Richard     | Reg. No. <u>-P-43,352</u> |
| Glance, Robert J.       | Reg. No. <u>40,620</u>   | Sumner, John P.        | Reg. No. <u>29,114</u>    |
| Golla, Charles E.       | Reg. No. <u>26,896</u>   | Sumners, John S.       | Reg. No. <u>24,216</u>    |
| Gorman, Alan G.         | Reg. No. <u>38,472</u>   | Tellekson, David K.    | Reg. No. <u>32,314</u>    |
| Gould, John D.          | Reg. No. <u>18,223</u>   | Trembath, Jon R.       | Reg. No. <u>38,344</u>    |
| Gregson, Richard        | Reg. No. <u>P-41,804</u> | Underhill, Albert L.   | Reg. No. <u>27,403</u>    |
| Gresens, John J.        | Reg. No. <u>33,112</u>   | Vandenburgh, J. Derek  | Reg. No. <u>32,179</u>    |
| Hamre, Curtis B.        | Reg. No. <u>29,165</u>   | Victor, David W.       | Reg. No. <u>39,867</u>    |
| Hillson, Randall A.     | Reg. No. <u>31,838</u>   | Welter, Paul A.        | Reg. No. <u>20,890</u>    |
| Johnston, Scott W.      | Reg. No. <u>39,721</u>   | Whipps, Brian          | Reg. No. <u>P-43,261</u>  |
| Kastelic, Joseph M.     | Reg. No. <u>37,160</u>   | Williams, Douglas J.   | Reg. No. <u>27,054</u>    |
| Kettelberger, Denise    | Reg. No. <u>33,924</u>   | Witt McDonald, Jonelle | Reg. No. <u>P-41,980</u>  |
| Komanduri, Janaki       | Reg. No. <u>40,684</u>   | Wood, Gregory B.       | Reg. No. <u>28,133</u>    |
| Kowalchyk, Alan W.      | Reg. No. <u>31,535</u>   | Wood, William J.       | Reg. No. <u>P-42,236</u>  |
| Kowalchyk, Katherine M. | Reg. No. <u>36,848</u>   | Xu, Min S.             | Reg. No. <u>39,536</u>    |
| Lacy, Paul E.           | Reg. No. <u>38,946</u>   |                        |                           |
| Larson, James A.        | Reg. No. <u>40,443</u>   |                        |                           |

I hereby authorize them to act and rely on instructions from and communicate directly with the person/assignee/attorney/firm/ organization who/which first sends/sent this case to them and by whom/which I hereby declare that I have consented after full disclosure to be represented unless/until I instruct Merchant, Gould, Smith, Edell, Welter & Schmidt to the contrary.

Please direct all correspondence in this case to Merchant, Gould, Smith, Edell, Welter & Schmidt at the address indicated below:

Merchant, Gould, Smith, Edell,  
Welter & Schmidt  
3100 Norwest Center  
90 South Seventh Street  
Minneapolis, MN 55402-4131

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

|                            |                                  |                                                                                 |                                          |                                                     |
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| Signature of Inventor 201: |                                  |                                                                                 | Date: 4-10-98                            |                                                     |
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| Signature of Inventor 203: |                                  |                                                                                 | Date: 4.6.98                             |                                                     |
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| Signature of Inventor 204: |                                  |                                                                                 | Date: 4.6.98                             |                                                     |

**§ 1.56 Duty to disclose information material to patentability.**

(a) A patent by its very nature is affected with a public interest. The public interest is best served, and the most effective patent examination occurs when, at the time an application is being examined, the Office is aware of and evaluates the teachings of all information material to patentability. Each individual associated with the filing and prosecution of a patent application has a duty of candor and good faith in dealing with the Office, which includes a duty to disclose to the Office all information known to that individual to be material to patentability as defined in this section. The duty to disclose information exists with respect to each pending claim until the claim is canceled or withdrawn from consideration, or the application becomes abandoned. Information material to the patentability of a claim that is canceled or withdrawn from consideration need not be submitted if the information is not material to the patentability of any claim remaining under consideration in the application. There is no duty to submit information which is not material to the patentability of any existing claim. The duty to disclose all information known to be material to patentability is deemed to be satisfied if all information known to be material to patentability of any claim issued in a patent was cited by the Office or submitted to the Office in the manner prescribed by §§ 1.97(b)-(d) and 1.98. However, no patent will be granted on an application in connection with which fraud on the Office was practiced or attempted or the duty of disclosure was violated through bad faith or intentional misconduct. The Office encourages applicants to carefully examine:

(1) prior art cited in search reports of a foreign patent office in a counterpart application, and

(2) the closest information over which individuals associated with the filing or prosecution of a patent application believe any pending claim patentably defines, to make sure that any material information contained therein is disclosed to the Office.

(b) Under this section, information is material to patentability when it is not cumulative to information already of record or being made of record in the application, and

(1) It establishes, by itself or in combination with other information, a prima facie case of unpatentability of a claim;

(2) It refutes, or is inconsistent with, a position the applicant takes in:

(i) Opposing an argument of unpatentability relied on by the Office, or

(ii) Asserting an argument of patentability.

A prima facie case of unpatentability is established when the information compels a conclusion that a claim is unpatentable under the preponderance of evidence, burden-of-proof standard, giving each term in the claim its broadest reasonable construction consistent with the specification, and before any consideration is given to evidence which may be submitted in an attempt to establish a contrary conclusion of patentability.

(c) Individuals associated with the filing or prosecution of a patent application within the meaning of this section are:

(1) Each inventor named in the application:

(2) Each attorney or agent who prepares or prosecutes the application; and

(3) Every other person who is substantively involved in the preparation or prosecution of the application and who is associated with the inventor, with the assignee or with anyone to whom there is an obligation to assign the application.

(d) Individuals other than the attorney, agent or inventor may comply with this section by disclosing information to the attorney, agent, or inventor.

## SEQUENCE LISTING

<110> Tsilibary, Photini-Effie  
 Charonis, Aristidis S.  
 Setty, Suman  
 Mauer, Michael

<120> ANALYSIS OF ALPHA INTEGRINS FOR THE DIAGNOSIS OF DIABETIC NEPHROPATHY

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<160> 16

<170> PatentIn version 3.1

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 <211> 3989  
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 <213> Rattus

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 <222> (420)..(3959)  
 <223>

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 accctcggag accacacgag tgaccagag cgcaagtgcg cagcgtcccg gttctgcctg 360  
 ttctgccag ctctgccca cgaaccggca cgtagctggt tccagcagcc gctccagca 419  
 atg gtc ccc agg cgt cct gcc agc cta gag gtc act gta gcc tgc ata 467  
 Met Val Pro Arg Arg Pro Ala Ser Leu Glu Val Thr Val Ala Cys Ile  
 1 5 10 15

|                                                                 |      |
|-----------------------------------------------------------------|------|
| tgg ctt ctc acg gtc atc cta ggc ttc tgc gtc tcc ttc aat gtt gat | 515  |
| Trp Leu Leu Thr Val Ile Leu Gly Phe Cys Val Ser Phe Asn Val Asp |      |
| 20 25 30                                                        |      |
| gtg aaa aac tca atg agt ttc agt ggc cca gta gag gac atg ttt gga | 563  |
| Val Lys Asn Ser Met Ser Phe Ser Gly Pro Val Glu Asp Met Phe Gly |      |
| 35 40 45                                                        |      |
| tac act gtt caa caa tat gaa aac gaa gaa ggc aaa tgg gtt ctt att | 611  |
| Tyr Thr Val Gln Gln Tyr Glu Asn Glu Glu Gly Lys Trp Val Leu Ile |      |
| 50 55 60                                                        |      |
| ggc tct cct tta gtt ggc caa ccc aaa gca aga act gga gat gtc tat | 659  |
| Gly Ser Pro Leu Val Gly Gln Pro Lys Ala Arg Thr Gly Asp Val Tyr |      |
| 65 70 75 80                                                     |      |
| aag tgt ccg gtt ggg aga gag aga gca atg cct tgc gtg aag ttg gac | 707  |
| Lys Cys Pro Val Gly Arg Glu Arg Ala Met Pro Cys Val Lys Leu Asp |      |
| 85 90 95                                                        |      |
| ttg cca gtt aac aca tcg atc ccc aat gtc aca gaa ata aag gaa aac | 755  |
| Leu Pro Val Asn Thr Ser Ile Pro Asn Val Thr Glu Ile Lys Glu Asn |      |
| 100 105 110                                                     |      |
| atg aca ttt gga tca act tta gtc acc aac ccg aat gga gga ttt ctg | 803  |
| Met Thr Phe Gly Ser Thr Leu Val Thr Asn Pro Asn Gly Gly Phe Leu |      |
| 115 120 125                                                     |      |
| gca tgt ggg ccc ttg tat gcc tat aga tgt gga cat ttg cat tat aca | 851  |
| Ala Cys Gly Pro Leu Tyr Ala Tyr Arg Cys Gly His Leu His Tyr Thr |      |
| 130 135 140                                                     |      |
| act gga ata tgt tct gat gtc agt cct aca ttt caa gtt gtg aac tcc | 899  |
| Thr Gly Ile Cys Ser Asp Val Ser Pro Thr Phe Gln Val Val Asn Ser |      |
| 145 150 155 160                                                 |      |
| ttt gcc cct gta caa gaa tgc agc acc cag ctg gac ata gtc atc gtc | 947  |
| Phe Ala Pro Val Gln Glu Cys Ser Thr Gln Leu Asp Ile Val Ile Val |      |
| 165 170 175                                                     |      |
| ctg gat ggc tcc aac agc atc tac ccc tgg gaa agt gtc atc gcc ttt | 995  |
| Leu Asp Gly Ser Asn Ser Ile Tyr Pro Trp Glu Ser Val Ile Ala Phe |      |
| 180 185 190                                                     |      |
| tta aac gac ctt ctt aag agg atg gat att ggc cct aag cag aca cag | 1043 |
| Leu Asn Asp Leu Leu Lys Arg Met Asp Ile Gly Pro Lys Gln Thr Gln |      |
| 195 200 205                                                     |      |
| gtc ggg att gta cag tat gga gag aat gta acc cat gag ttc aac ctc | 1091 |
| Val Gly Ile Val Gln Tyr Gly Glu Asn Val Thr His Glu Phe Asn Leu |      |
| 210 215 220                                                     |      |
| aat aag tat tca tcc aca gaa gag gtc ctt gtc gca gca aac aaa ata | 1139 |
| Asn Lys Tyr Ser Ser Thr Glu Glu Val Leu Val Ala Ala Asn Lys Ile |      |
| 225 230 235 240                                                 |      |
| ggc cga cag gga ggc ctc caa acg atg aca gcc ctt gga ata gac aca | 1187 |
| Gly Arg Gln Gly Gly Leu Gln Thr Met Thr Ala Leu Gly Ile Asp Thr |      |
| 245 250 255                                                     |      |



|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| gcc agg aaa gag gca ttc act gaa gct cgg ggt gcc agg agg gga gtt<br>Ala Arg Lys Glu Ala Phe Thr Glu Ala Arg Gly Ala Arg Arg Gly Val<br>260 265 270     | 1235 |
| aaa aaa gtc atg gtt att gtg acc gac gga gaa tcg cat gac aac tat<br>Lys Lys Val Met Val Ile Val Thr Asp Gly Glu Ser His Asp Asn Tyr<br>275 280 285     | 1283 |
| cgc ctg aaa cag gtc atc caa gac tgc gag gac gaa aac att cag cga<br>Arg Leu Lys Gln Val Ile Gln Asp Cys Glu Asp Glu Asn Ile Gln Arg<br>290 295 300     | 1331 |
| ttt tcc ata gct atc ctt ggc cac tat aac agg ggg aac tta agc act<br>Phe Ser Ile Ala Ile Leu Gly His Tyr Asn Arg Gly Asn Leu Ser Thr<br>305 310 315 320 | 1379 |
| gaa aaa ttt gtg gag gaa ata aaa tcg atc gca agc gag ccc acg gaa<br>Glu Lys Phe Val Glu Glu Ile Lys Ser Ile Ala Ser Glu Pro Thr Glu<br>325 330 335     | 1427 |
| aag cac ttc ttc aat gtc tcg gat gag ttg gcc ctg gtc act att gtt<br>Lys His Phe Phe Asn Val Ser Asp Glu Leu Ala Leu Val Thr Ile Val<br>340 345 350     | 1475 |
| aaa gct ctg gga gaa agg ata ttc gct ttg gaa gcg aca gct gac cag<br>Lys Ala Leu Gly Glu Arg Ile Phe Ala Leu Glu Ala Thr Ala Asp Gln<br>355 360 365     | 1523 |
| tca gca gct tca ttt gag atg gaa atg tct cag act ggc ttc agt gct<br>Ser Ala Ala Ser Phe Glu Met Glu Met Ser Gln Thr Gly Phe Ser Ala<br>370 375 380     | 1571 |
| cac tac tcc cag gac tgg gtc atg ctt gga gcg gtg gga gcc tat gac<br>His Tyr Ser Gln Asp Trp Val Met Leu Gly Ala Val Gly Ala Tyr Asp<br>385 390 395 400 | 1619 |
| tgg aac gga act gtg gtc atg cag aag gct aac cag atg gtc atc cct<br>Trp Asn Gly Thr Val Val Met Gln Lys Ala Asn Gln Met Val Ile Pro<br>405 410 415     | 1667 |
| cat aac acc acc ttt caa act gag ccc gcc aag atg aac gag cct ctg<br>His Asn Thr Thr Phe Gln Thr Glu Pro Ala Lys Met Asn Glu Pro Leu<br>420 425 430     | 1715 |
| gct tct tat tta ggt tac aca gtg aac tcg gcc acc atc cct gga gat<br>Ala Ser Tyr Leu Gly Tyr Thr Val Asn Ser Ala Thr Ile Pro Gly Asp<br>435 440 445     | 1763 |
| gtg ctc tac atc gct ggg cag cct cgg tac aat cat acg ggc cag gtc<br>Val Leu Tyr Ile Ala Gly Gln Pro Arg Tyr Asn His Thr Gly Gln Val<br>450 455 460     | 1811 |
| gtc atc tac aag atg gag gat ggg aac atc aac att ctg cag aca ctc<br>Val Ile Tyr Lys Met Glu Asp Gly Asn Ile Asn Ile Leu Gln Thr Leu<br>465 470 475 480 | 1859 |
| ggc gga gag cag att ggt tcc tac ttt ggt agt gtc tta aca aca att<br>Gly Gly Glu Gln Ile Gly Ser Tyr Phe Gly Ser Val Leu Thr Thr Ile<br>485 490 495     | 1907 |

|                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |      |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| gac<br>Asp        | atc<br>Ile        | gac<br>Asp        | aaa<br>Lys<br>500 | gat<br>Asp        | tct<br>Ser        | tat<br>Tyr        | act<br>Thr        | gat<br>Asp<br>505 | ctg<br>Leu        | ctt<br>Leu        | ctc<br>Leu        | gtc<br>Val        | ggg<br>Gly<br>510 | gcc<br>Ala        | ccc<br>Pro        | 1955 |
| atg<br>Met        | tac<br>Tyr        | atg<br>Met<br>515 | ggg<br>Gly        | aca<br>Thr        | gag<br>Glu        | aaa<br>Lys        | gag<br>Glu<br>520 | gaa<br>Glu        | cag<br>Gln        | ggc<br>Gly        | aag<br>Lys        | gtg<br>Val<br>525 | tac<br>Tyr        | gtg<br>Val        | tac<br>Tyr        | 2003 |
| gct<br>Ala        | gtg<br>Val<br>530 | aat<br>Asn        | cag<br>Gln        | aca<br>Thr        | agg<br>Arg        | ttt<br>Phe<br>535 | gaa<br>Glu        | tat<br>Tyr        | caa<br>Gln        | atg<br>Met        | agc<br>Ser<br>540 | ctg<br>Leu        | gaa<br>Glu        | cca<br>Pro        | att<br>Ile        | 2051 |
| agg<br>Arg<br>545 | cag<br>Gln        | acc<br>Thr        | tgc<br>Cys        | tgc<br>Cys        | tca<br>Ser<br>550 | tcc<br>Ser        | ctg<br>Leu        | aag<br>Lys        | gat<br>Asp        | aat<br>Asn<br>555 | tca<br>Ser        | tgc<br>Cys        | acg<br>Thr        | aaa<br>Lys        | gaa<br>Glu<br>560 | 2099 |
| aac<br>Asn        | aag<br>Lys        | aat<br>Asn        | gag<br>Glu        | ccc<br>Pro<br>565 | tgc<br>Cys        | ggg<br>Gly        | gcc<br>Ala        | cgc<br>Arg        | ttc<br>Phe<br>570 | gga<br>Gly        | aca<br>Thr        | gca<br>Ala        | att<br>Ile<br>575 | gct<br>Ala        | gct<br>Ala        | 2147 |
| gta<br>Val        | aaa<br>Lys        | gac<br>Asp        | ctc<br>Leu<br>580 | aac<br>Asn        | gtg<br>Val        | gat<br>Asp        | gga<br>Gly<br>585 | ttt<br>Phe        | aat<br>Asn        | gac<br>Asp        | gtc<br>Val        | gtg<br>Val        | att<br>Ile<br>590 | gga<br>Gly        | gct<br>Ala        | 2195 |
| ccg<br>Pro        | ctg<br>Leu        | gaa<br>Glu<br>595 | gat<br>Asp        | gac<br>Asp        | cac<br>His        | gca<br>Ala        | gga<br>Gly<br>600 | gct<br>Ala        | gtg<br>Val        | tac<br>Tyr        | att<br>Ile        | tat<br>Tyr<br>605 | cat<br>His        | ggc<br>Gly        | agt<br>Ser        | 2243 |
| ggc<br>Gly<br>610 | aag<br>Lys        | acc<br>Thr        | ata<br>Ile        | agg<br>Arg        | gag<br>Glu        | gcg<br>Ala<br>615 | tat<br>Tyr        | gca<br>Ala        | caa<br>Gln        | cgc<br>Arg        | att<br>Ile<br>620 | cca<br>Pro        | tca<br>Ser        | ggt<br>Gly        | ggg<br>Gly        | 2291 |
| gat<br>Asp<br>625 | ggc<br>Gly        | aag<br>Lys        | acc<br>Thr        | ctg<br>Leu        | aaa<br>Lys<br>630 | ttt<br>Phe        | ttc<br>Phe        | ggc<br>Gly        | cag<br>Gln        | tct<br>Ser<br>635 | atc<br>Ile        | cac<br>His        | gga<br>Gly        | gag<br>Glu        | atg<br>Met<br>640 | 2339 |
| gat<br>Asp        | tta<br>Leu        | aat<br>Asn        | ggt<br>Gly        | gac<br>Asp<br>645 | ggt<br>Gly        | ctg<br>Leu        | act<br>Thr        | gac<br>Asp        | gtg<br>Val<br>650 | acc<br>Thr        | att<br>Ile        | gga<br>Gly        | ggc<br>Gly        | ctt<br>Leu<br>655 | ggt<br>Gly        | 2387 |
| gga<br>Gly        | gca<br>Ala        | gcc<br>Ala        | ctc<br>Leu<br>660 | ttc<br>Phe        | tgg<br>Trp        | gcc<br>Ala        | aga<br>Arg        | gat<br>Asp<br>665 | gtg<br>Val        | gct<br>Ala        | gta<br>Val        | gtt<br>Val<br>670 | aaa<br>Lys        | gtg<br>Val        | acc<br>Thr        | 2435 |
| atg<br>Met        | aat<br>Asn        | ttt<br>Phe<br>675 | gaa<br>Glu        | ccc<br>Pro        | aat<br>Asn        | aaa<br>Lys        | gtg<br>Val<br>680 | aat<br>Asn        | att<br>Ile        | caa<br>Gln        | aag<br>Lys        | aaa<br>Lys<br>685 | aac<br>Asn        | tgc<br>Cys        | cgt<br>Arg        | 2483 |
| gtg<br>Val        | gag<br>Glu<br>690 | ggc<br>Gly        | aaa<br>Lys        | gaa<br>Glu        | aca<br>Thr        | gtg<br>Val<br>695 | tgc<br>Cys        | ata<br>Ile        | aat<br>Asn        | gct<br>Ala        | aca<br>Thr<br>700 | atg<br>Met        | tgt<br>Cys        | ttt<br>Phe        | cat<br>His        | 2531 |
| gtg<br>Val<br>705 | aaa<br>Lys        | tta<br>Leu        | aag<br>Lys        | tct<br>Ser        | aaa<br>Lys<br>710 | gag<br>Glu        | gac<br>Asp        | tca<br>Ser        | att<br>Ile        | tac<br>Tyr<br>715 | gag<br>Glu        | gct<br>Ala        | gat<br>Asp        | ctg<br>Leu        | cag<br>Gln<br>720 | 2579 |
| tac<br>Tyr        | cgt<br>Arg        | gtc<br>Val        | acc<br>Thr        | ctt<br>Leu<br>725 | gat<br>Asp        | tca<br>Ser        | ctg<br>Leu        | agg<br>Arg        | cag<br>Gln<br>730 | ata<br>Ile        | tca<br>Ser        | cgg<br>Arg        | agc<br>Ser        | ttt<br>Phe<br>735 | ttt<br>Phe        | 2627 |

|                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |      |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| tct<br>Ser        | gga<br>Gly        | act<br>Thr        | cag<br>Gln<br>740 | gaa<br>Glu        | agg<br>Arg        | aag<br>Lys        | att<br>Ile        | caa<br>Gln<br>745 | aga<br>Arg        | aat<br>Asn        | atc<br>Ile        | acc<br>Thr        | gtt<br>Val<br>750 | cga<br>Arg        | gaa<br>Glu        | 2675 |
| tca<br>Ser        | gaa<br>Glu        | tgc<br>Cys<br>755 | atc<br>Ile        | agg<br>Arg        | cac<br>His        | tcc<br>Ser        | ttc<br>Phe<br>760 | tac<br>Tyr        | atg<br>Met        | ttg<br>Leu        | gac<br>Asp        | aaa<br>Lys<br>765 | cat<br>His        | gac<br>Asp        | ttt<br>Phe        | 2723 |
| cag<br>Gln        | gac<br>Asp<br>770 | tct<br>Ser        | gtg<br>Val        | aga<br>Arg        | gtg<br>Val        | act<br>Thr<br>775 | ctg<br>Leu        | gat<br>Asp        | ttt<br>Phe        | aat<br>Asn        | ctc<br>Leu<br>780 | act<br>Thr        | gat<br>Asp        | cca<br>Pro        | gaa<br>Glu        | 2771 |
| aat<br>Asn<br>785 | ggt<br>Gly        | cct<br>Pro        | gta<br>Val        | ctt<br>Leu        | gat<br>Asp<br>790 | gac<br>Asp        | gct<br>Ala        | ctg<br>Leu        | cca<br>Pro        | aac<br>Asn<br>795 | tca<br>Ser        | gtc<br>Val        | cac<br>His        | gaa<br>Glu        | cac<br>His<br>800 | 2819 |
| att<br>Ile        | ccc<br>Pro        | ttt<br>Phe        | gcc<br>Ala        | aaa<br>Lys<br>805 | gac<br>Asp        | tgt<br>Cys        | gga<br>Gly        | aac<br>Asn        | aag<br>Lys<br>810 | gaa<br>Glu        | aga<br>Arg        | tgc<br>Cys        | att<br>Ile        | tca<br>Ser        | gac<br>Asp<br>815 | 2867 |
| ctc<br>Leu        | act<br>Thr        | ctg<br>Leu        | aat<br>Asn<br>820 | gtg<br>Val        | tcc<br>Ser        | acc<br>Thr        | aca<br>Thr        | gaa<br>Glu<br>825 | aag<br>Lys        | agc<br>Ser        | ctg<br>Leu        | ctg<br>Leu        | atc<br>Ile<br>830 | gtc<br>Val        | aag<br>Lys        | 2915 |
| tcc<br>Ser        | cag<br>Gln        | cat<br>His<br>835 | gac<br>Asp        | aag<br>Lys        | ttc<br>Phe        | aac<br>Asn        | gtt<br>Val<br>840 | agc<br>Ser        | ctc<br>Leu        | acc<br>Thr        | gtc<br>Val        | aaa<br>Lys<br>845 | aac<br>Asn        | aaa<br>Lys        | gga<br>Gly        | 2963 |
| gac<br>Asp        | agt<br>Ser<br>850 | gcg<br>Ala        | tac<br>Tyr        | aac<br>Asn        | acc<br>Thr        | agg<br>Arg<br>855 | aca<br>Thr        | gtg<br>Val        | gtg<br>Val        | cag<br>Gln        | cat<br>His<br>860 | tca<br>Ser        | cca<br>Pro        | aat<br>Asn        | ctg<br>Leu        | 3011 |
| att<br>Ile<br>865 | ttt<br>Phe        | tcg<br>Ser        | gga<br>Gly        | att<br>Ile        | gag<br>Glu<br>870 | gag<br>Glu        | atc<br>Ile        | caa<br>Gln        | aaa<br>Lys        | gat<br>Asp<br>875 | agc<br>Ser        | tgt<br>Cys        | gaa<br>Glu        | tct<br>Ser        | aat<br>Asn<br>880 | 3059 |
| caa<br>Gln        | aat<br>Asn        | atc<br>Ile        | act<br>Thr        | tgc<br>Cys<br>885 | aga<br>Arg        | gtt<br>Val        | gga<br>Gly        | tat<br>Tyr        | cct<br>Pro<br>890 | ttc<br>Phe        | cta<br>Leu        | aga<br>Arg        | gca<br>Ala        | gga<br>Gly<br>895 | gaa<br>Glu        | 3107 |
| acg<br>Thr        | gtt<br>Val        | acc<br>Thr        | ttc<br>Phe<br>900 | aaa<br>Lys        | ata<br>Ile        | ata<br>Ile        | ttc<br>Phe        | cag<br>Gln<br>905 | ttt<br>Phe        | aac<br>Asn        | aca<br>Thr        | tcc<br>Ser        | cat<br>His<br>910 | ctc<br>Leu        | tcg<br>Ser        | 3155 |
| gaa<br>Glu        | aat<br>Asn        | gca<br>Ala<br>915 | atc<br>Ile        | att<br>Ile        | cac<br>His        | tta<br>Leu        | agt<br>Ser<br>920 | gca<br>Ala        | aca<br>Thr        | agt<br>Ser        | gac<br>Asp        | agt<br>Ser<br>925 | gag<br>Glu        | gag<br>Glu        | ccc<br>Pro        | 3203 |
| ctg<br>Leu        | gaa<br>Glu<br>930 | tct<br>Ser        | ctt<br>Leu        | aat<br>Asn        | gat<br>Asp        | aat<br>Asn<br>935 | gaa<br>Glu        | gta<br>Val        | aat<br>Asn        | att<br>Ile        | tcc<br>Ser<br>940 | atc<br>Ile        | cca<br>Pro        | gta<br>Val        | aaa<br>Lys        | 3251 |
| tat<br>Tyr<br>945 | gaa<br>Glu        | gtt<br>Val        | gga<br>Gly        | ctg<br>Leu        | cag<br>Gln<br>950 | ttt<br>Phe        | tac<br>Tyr        | agt<br>Ser        | tct<br>Ser        | gcg<br>Ala<br>955 | agt<br>Ser        | gaa<br>Glu        | cat<br>His        | cac<br>His        | att<br>Ile<br>960 | 3299 |
| tca<br>Ser        | gtc<br>Val        | gct<br>Ala        | gcc<br>Ala        | aat<br>Asn<br>965 | gag<br>Glu        | acg<br>Thr        | atc<br>Ile        | cct<br>Pro        | gag<br>Glu<br>970 | ttt<br>Phe        | att<br>Ile        | aac<br>Asn        | tcc<br>Ser        | act<br>Thr<br>975 | gag<br>Glu        | 3347 |



<213> Rattus

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Val Lys Asn Ser Met Ser Phe Ser Gly Pro Val Glu Asp Met Phe Gly  
35 40 45

Tyr Thr Val Gln Gln Tyr Glu Asn Glu Glu Gly Lys Trp Val Leu Ile  
50 55 60

Gly Ser Pro Leu Val Gly Gln Pro Lys Ala Arg Thr Gly Asp Val Tyr  
65 70 75 80

Lys Cys Pro Val Gly Arg Glu Arg Ala Met Pro Cys Val Lys Leu Asp  
85 90 95

Leu Pro Val Asn Thr Ser Ile Pro Asn Val Thr Glu Ile Lys Glu Asn  
100 105 110

Met Thr Phe Gly Ser Thr Leu Val Thr Asn Pro Asn Gly Gly Phe Leu  
115 120 125

Ala Cys Gly Pro Leu Tyr Ala Tyr Arg Cys Gly His Leu His Tyr Thr  
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Thr Gly Ile Cys Ser Asp Val Ser Pro Thr Phe Gln Val Val Asn Ser  
145 150 155 160

Phe Ala Pro Val Gln Glu Cys Ser Thr Gln Leu Asp Ile Val Ile Val  
165 170 175

Leu Asp Gly Ser Asn Ser Ile Tyr Pro Trp Glu Ser Val Ile Ala Phe  
180 185 190

Leu Asn Asp Leu Leu Lys Arg Met Asp Ile Gly Pro Lys Gln Thr Gln  
195 200 205

Val Gly Ile Val Gln Tyr Gly Glu Asn Val Thr His Glu Phe Asn Leu  
210 215 220

Asn Lys Tyr Ser Ser Thr Glu Glu Val Leu Val Ala Ala Asn Lys Ile  
 225 230 235 240

Gly Arg Gln Gly Gly Leu Gln Thr Met Thr Ala Leu Gly Ile Asp Thr  
 245 250 255

Ala Arg Lys Glu Ala Phe Thr Glu Ala Arg Gly Ala Arg Arg Gly Val  
 260 265 270

Lys Lys Val Met Val Ile Val Thr Asp Gly Glu Ser His Asp Asn Tyr  
 275 280 285

Arg Leu Lys Gln Val Ile Gln Asp Cys Glu Asp Glu Asn Ile Gln Arg  
 290 295 300

Phe Ser Ile Ala Ile Leu Gly His Tyr Asn Arg Gly Asn Leu Ser Thr  
 305 310 315 320

Glu Lys Phe Val Glu Glu Ile Lys Ser Ile Ala Ser Glu Pro Thr Glu  
 325 330 335

Lys His Phe Phe Asn Val Ser Asp Glu Leu Ala Leu Val Thr Ile Val  
 340 345 350

Lys Ala Leu Gly Glu Arg Ile Phe Ala Leu Glu Ala Thr Ala Asp Gln  
 355 360 365

Ser Ala Ala Ser Phe Glu Met Glu Met Ser Gln Thr Gly Phe Ser Ala  
 370 375 380

His Tyr Ser Gln Asp Trp Val Met Leu Gly Ala Val Gly Ala Tyr Asp  
 385 390 395 400

Trp Asn Gly Thr Val Val Met Gln Lys Ala Asn Gln Met Val Ile Pro  
 405 410 415

His Asn Thr Thr Phe Gln Thr Glu Pro Ala Lys Met Asn Glu Pro Leu  
 420 425 430

Ala Ser Tyr Leu Gly Tyr Thr Val Asn Ser Ala Thr Ile Pro Gly Asp  
 435 440 445

Val Leu Tyr Ile Ala Gly Gln Pro Arg Tyr Asn His Thr Gly Gln Val  
 450 455 460

Val Ile Tyr Lys Met Glu Asp Gly Asn Ile Asn Ile Leu Gln Thr Leu  
465 470 475 480

Gly Gly Glu Gln Ile Gly Ser Tyr Phe Gly Ser Val Leu Thr Thr Ile  
485 490 495

Asp Ile Asp Lys Asp Ser Tyr Thr Asp Leu Leu Leu Val Gly Ala Pro  
500 505 510

Met Tyr Met Gly Thr Glu Lys Glu Glu Gln Gly Lys Val Tyr Val Tyr  
515 520 525

Ala Val Asn Gln Thr Arg Phe Glu Tyr Gln Met Ser Leu Glu Pro Ile  
530 535 540

Arg Gln Thr Cys Cys Ser Ser Leu Lys Asp Asn Ser Cys Thr Lys Glu  
545 550 555 560

Asn Lys Asn Glu Pro Cys Gly Ala Arg Phe Gly Thr Ala Ile Ala Ala  
565 570 575

Val Lys Asp Leu Asn Val Asp Gly Phe Asn Asp Val Val Ile Gly Ala  
580 585 590

Pro Leu Glu Asp Asp His Ala Gly Ala Val Tyr Ile Tyr His Gly Ser  
595 600 605

Gly Lys Thr Ile Arg Glu Ala Tyr Ala Gln Arg Ile Pro Ser Gly Gly  
610 615 620

Asp Gly Lys Thr Leu Lys Phe Phe Gly Gln Ser Ile His Gly Glu Met  
625 630 635 640

Asp Leu Asn Gly Asp Gly Leu Thr Asp Val Thr Ile Gly Gly Leu Gly  
645 650 655

Gly Ala Ala Leu Phe Trp Ala Arg Asp Val Ala Val Val Lys Val Thr  
660 665 670

Met Asn Phe Glu Pro Asn Lys Val Asn Ile Gln Lys Lys Asn Cys Arg  
675 680 685

Val Glu Gly Lys Glu Thr Val Cys Ile Asn Ala Thr Met Cys Phe His  
690 695 700

Val Lys Leu Lys Ser Lys Glu Asp Ser Ile Tyr Glu Ala Asp Leu Gln  
705 710 715 720

Tyr Arg Val Thr Leu Asp Ser Leu Arg Gln Ile Ser Arg Ser Phe Phe  
725 730 735

Ser Gly Thr Gln Glu Arg Lys Ile Gln Arg Asn Ile Thr Val Arg Glu  
740 745 750

Ser Glu Cys Ile Arg His Ser Phe Tyr Met Leu Asp Lys His Asp Phe  
755 760 765

Gln Asp Ser Val Arg Val Thr Leu Asp Phe Asn Leu Thr Asp Pro Glu  
770 775 780

Asn Gly Pro Val Leu Asp Asp Ala Leu Pro Asn Ser Val His Glu His  
785 790 795 800

Ile Pro Phe Ala Lys Asp Cys Gly Asn Lys Glu Arg Cys Ile Ser Asp  
805 810 815

Leu Thr Leu Asn Val Ser Thr Thr Glu Lys Ser Leu Leu Ile Val Lys  
820 825 830

Ser Gln His Asp Lys Phe Asn Val Ser Leu Thr Val Lys Asn Lys Gly  
835 840 845

Asp Ser Ala Tyr Asn Thr Arg Thr Val Val Gln His Ser Pro Asn Leu  
850 855 860

Ile Phe Ser Gly Ile Glu Glu Ile Gln Lys Asp Ser Cys Glu Ser Asn  
865 870 875 880

Gln Asn Ile Thr Cys Arg Val Gly Tyr Pro Phe Leu Arg Ala Gly Glu  
885 890 895

Thr Val Thr Phe Lys Ile Ile Phe Gln Phe Asn Thr Ser His Leu Ser  
900 905 910

Glu Asn Ala Ile Ile His Leu Ser Ala Thr Ser Asp Ser Glu Glu Pro  
915 920 925

Leu Glu Ser Leu Asn Asp Asn Glu Val Asn Ile Ser Ile Pro Val Lys  
930 935 940



Tyr Glu Val Gly Leu Gln Phe Tyr Ser Ser Ala Ser Glu His His Ile  
 945 950 955 960

Ser Val Ala Ala Asn Glu Thr Ile Pro Glu Phe Ile Asn Ser Thr Glu  
 965 970 975

Asp Ile Gly Asn Glu Ile Asn Val Phe Tyr Thr Ile Arg Lys Arg Gly  
 980 985 990

His Phe Pro Met Pro Glu Leu Gln Leu Ser Ile Ser Phe Pro Asn Leu  
 995 1000 1005

Thr Ala Asp Gly Tyr Pro Val Leu Tyr Pro Ile Gly Trp Ser Ser  
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Ser Asp Asn Val Asn Cys Arg Pro Arg Ser Leu Glu Asp Pro Phe  
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Gly Ile Asn Ser Gly Lys Lys Met Thr Ile Ser Lys Ser Glu Val  
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Leu Lys Arg Gly Thr Ile Gln Asp Cys Ser Ser Thr Cys Gly Val  
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Ala Thr Ile Thr Cys Ser Leu Leu Pro Ser Asp Leu Ser Gln Val  
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Asn Val Ser Leu Leu Leu Trp Lys Pro Thr Phe Ile Arg Ala His  
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Phe Ser Ser Leu Asn Leu Thr Leu Arg Gly Glu Leu Lys Ser Glu  
 1100 1105 1110

Asn Ser Ser Leu Thr Leu Ser Ser Ser Asn Arg Lys Arg Glu Leu  
 1115 1120 1125

Ala Ile Gln Ile Ser Lys Asp Gly Leu Pro Gly Arg Val Pro Leu  
 1130 1135 1140

Trp Val Ile Leu Leu Ser Ala Phe Ala Gly Leu Leu Leu Leu Met  
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 Glu Arg Thr Gly Ala Ala Pro Leu Pro Leu Leu Leu Val Leu Ala Leu  
 5 10 15

agt caa ggc att tta aat tgt tgt ttg gcc tac aat gtt ggt ctc cca 153  
 Ser Gln Gly Ile Leu Asn Cys Cys Leu Ala Tyr Asn Val Gly Leu Pro  
 20 25 30 35

gaa gca aaa ata ttt tcc ggt cct tca agt gaa cag ttt ggg tat gca 201  
 Glu Ala Lys Ile Phe Ser Gly Pro Ser Ser Glu Gln Phe Gly Tyr Ala  
 40 45 50

gtg cag cag ttt ata aat cca aaa ggc aac tgg tta ctg gtt ggt tca 249  
 Val Gln Gln Phe Ile Asn Pro Lys Gly Asn Trp Leu Leu Val Gly Ser  
 55 60 65

ccc tgg agt ggc ttt cct gag aac cga atg gga gat gtg tat aaa tgt 297  
 Pro Trp Ser Gly Phe Pro Glu Asn Arg Met Gly Asp Val Tyr Lys Cys  
 70 75 80

cct gtt gac cta tcc act gcc aca tgt gaa aaa cta aat ttg caa act 345  
 Pro Val Asp Leu Ser Thr Ala Thr Cys Glu Lys Leu Asn Leu Gln Thr  
 85 90 95

tca aca agc att cca aat gtt act gag atg aaa acc aac atg agc ctc 393  
 Ser Thr Ser Ile Pro Asn Val Thr Glu Met Lys Thr Asn Met Ser Leu  
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ggc ttg atc ctc acc agg aac atg gga act gga ggt ttt ctc aca tgt 441  
 Gly Leu Ile Leu Thr Arg Asn Met Gly Thr Gly Gly Phe Leu Thr Cys  
 120 125 130

ggt cct ctg tgg gca cag caa tgt ggg aat cag tat tac aca acg ggt 489  
 Gly Pro Leu Trp Ala Gln Gln Cys Gly Asn Gln Tyr Tyr Thr Thr Gly  
 135 140 145

gtg tgt tct gac atc agt cct gat ttt cag ctc tca gcc agc ttc tca 537  
 Val Cys Ser Asp Ile Ser Pro Asp Phe Gln Leu Ser Ala Ser Phe Ser  
 150 155 160





|                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |      |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| gtg<br>Val        | gtt<br>Val<br>645 | caa<br>Gln        | ctc<br>Leu        | tgg<br>Trp        | tca<br>Ser        | caa<br>Gln<br>650 | agt<br>Ser        | att<br>Ile        | gct<br>Ala        | gat<br>Asp        | gta<br>Val<br>655 | gct<br>Ala        | ata<br>Ile        | gaa<br>Glu        | gct<br>Ala        | 2025 |
| tca<br>Ser<br>660 | ttc<br>Phe        | aca<br>Thr        | cca<br>Pro        | gaa<br>Glu        | aaa<br>Lys<br>665 | atc<br>Ile        | act<br>Thr        | ttg<br>Leu        | gtc<br>Val        | aac<br>Asn<br>670 | aag<br>Lys        | aat<br>Asn        | gct<br>Ala        | cag<br>Gln        | ata<br>Ile<br>675 | 2073 |
| att<br>Ile        | ctc<br>Leu        | aaa<br>Lys        | ctc<br>Leu        | tgc<br>Cys<br>680 | ttc<br>Phe        | agt<br>Ser        | gca<br>Ala        | aag<br>Lys        | ttc<br>Phe<br>685 | aga<br>Arg        | cct<br>Pro        | act<br>Thr        | aag<br>Lys        | caa<br>Gln<br>690 | aac<br>Asn        | 2121 |
| aat<br>Asn        | caa<br>Gln        | gtg<br>Val        | gcc<br>Ala<br>695 | att<br>Ile        | gta<br>Val        | tat<br>Tyr        | aac<br>Asn        | atc<br>Ile<br>700 | aca<br>Thr        | ctt<br>Leu        | gat<br>Asp        | gca<br>Ala<br>705 | gat<br>Asp        | gga<br>Gly        | ttt<br>Phe        | 2169 |
| tca<br>Ser        | tcc<br>Ser<br>710 | aga<br>Arg        | gta<br>Val        | acc<br>Thr        | tcc<br>Ser        | agg<br>Arg        | ggg<br>Gly<br>715 | tta<br>Leu        | ttt<br>Phe        | aaa<br>Lys        | gaa<br>Glu        | aac<br>Asn<br>720 | aat<br>Asn        | gaa<br>Glu        | agg<br>Arg        | 2217 |
| tgc<br>Cys<br>725 | ctg<br>Leu        | cag<br>Gln        | aag<br>Lys        | aat<br>Asn        | atg<br>Met        | gta<br>Val<br>730 | gta<br>Val        | aat<br>Asn        | caa<br>Gln        | gca<br>Ala<br>735 | cag<br>Gln        | agt<br>Ser        | tgc<br>Cys        | ccc<br>Pro        | gag<br>Glu        | 2265 |
| cac<br>His<br>740 | atc<br>Ile        | att<br>Ile        | tat<br>Tyr        | ata<br>Ile        | cag<br>Gln<br>745 | gag<br>Glu        | ccc<br>Pro        | tct<br>Ser        | gat<br>Asp        | gtt<br>Val<br>750 | gtc<br>Val        | aac<br>Asn        | tct<br>Ser        | ttg<br>Leu        | gat<br>Asp<br>755 | 2313 |
| ttg<br>Leu        | cgt<br>Arg        | gtg<br>Val        | gac<br>Asp        | atc<br>Ile<br>760 | agt<br>Ser        | ctg<br>Leu        | gaa<br>Glu        | aac<br>Asn        | cct<br>Pro<br>765 | ggc<br>Gly        | act<br>Thr        | agc<br>Ser        | cct<br>Pro        | gcc<br>Ala<br>770 | ctt<br>Leu        | 2361 |
| gaa<br>Glu        | gcc<br>Ala        | tat<br>Tyr        | tct<br>Ser<br>775 | gag<br>Glu        | act<br>Thr        | gcc<br>Ala        | aag<br>Lys        | gtc<br>Val<br>780 | ttc<br>Phe        | agt<br>Ser        | att<br>Ile        | cct<br>Pro        | ttc<br>Phe<br>785 | cac<br>His        | aaa<br>Lys        | 2409 |
| gac<br>Asp        | tgt<br>Cys        | ggc<br>Gly<br>790 | gag<br>Glu        | gat<br>Asp        | gga<br>Gly        | ctt<br>Leu        | tgc<br>Cys<br>795 | att<br>Ile        | tct<br>Ser        | gat<br>Asp        | cta<br>Leu        | gtc<br>Val<br>800 | cta<br>Leu        | gat<br>Asp        | gtc<br>Val        | 2457 |
| cga<br>Arg        | caa<br>Gln<br>805 | ata<br>Ile        | cca<br>Pro        | gct<br>Ala        | gct<br>Ala        | caa<br>Gln<br>810 | gaa<br>Glu        | caa<br>Gln        | ccc<br>Pro        | ttt<br>Phe        | att<br>Ile<br>815 | gtc<br>Val        | agc<br>Ser        | aac<br>Asn        | caa<br>Gln        | 2505 |
| aac<br>Asn<br>820 | aaa<br>Lys        | agg<br>Arg        | tta<br>Leu        | aca<br>Thr        | ttt<br>Phe<br>825 | tca<br>Ser        | gta<br>Val        | aca<br>Thr        | ctg<br>Leu        | aaa<br>Lys<br>830 | aat<br>Asn        | aaa<br>Lys        | agg<br>Arg        | gaa<br>Glu        | agt<br>Ser<br>835 | 2553 |
| gca<br>Ala        | tac<br>Tyr        | aac<br>Asn        | act<br>Thr        | gga<br>Gly<br>840 | att<br>Ile        | gtt<br>Val        | gtt<br>Val        | gat<br>Asp        | ttt<br>Phe<br>845 | tca<br>Ser        | gaa<br>Glu        | aac<br>Asn        | ttg<br>Leu        | ttt<br>Phe<br>850 | ttt<br>Phe        | 2601 |
| gca<br>Ala        | tca<br>Ser        | ttc<br>Phe        | tcc<br>Ser<br>855 | cta<br>Leu        | ccg<br>Pro        | gtt<br>Val        | gat<br>Asp        | ggg<br>Gly<br>860 | aca<br>Thr        | gaa<br>Glu        | gta<br>Val        | aca<br>Thr        | tgc<br>Cys<br>865 | cag<br>Gln        | gtg<br>Val        | 2649 |
| gct<br>Ala        | gca<br>Ala        | tct<br>Ser<br>870 | cag<br>Gln        | aag<br>Lys        | tct<br>Ser        | gtt<br>Val<br>875 | gcc<br>Ala        | tgc<br>Cys        | gat<br>Asp        | gta<br>Val        | ggc<br>Gly<br>880 | tac<br>Tyr        | cct<br>Pro        | gct<br>Ala        | tta<br>Leu        | 2697 |

|                 |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
|-----------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|
| aag<br>Lys      | aga<br>Arg | gaa<br>Glu | caa<br>Gln | cag<br>Gln | gtg<br>Val | act<br>Thr | ttt<br>Phe | act<br>Thr | att<br>Ile | aac<br>Asn | ttt<br>Phe | gac<br>Asp | ttc<br>Phe | aat<br>Asn | ctt<br>Leu | 2745 |
| 885 890 895     |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| caa<br>Gln      | aac<br>Asn | ctt<br>Leu | cag<br>Gln | aat<br>Asn | cag<br>Gln | gcg<br>Ala | tct<br>Ser | ctc<br>Leu | agt<br>Ser | ttc<br>Phe | caa<br>Gln | gcc<br>Ala | tta<br>Leu | agt<br>Ser | gaa<br>Glu | 2793 |
| 900 905 910 915 |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| agc<br>Ser      | caa<br>Gln | gaa<br>Glu | gaa<br>Glu | aac<br>Asn | aag<br>Lys | gct<br>Ala | gat<br>Asp | aat<br>Asn | ttg<br>Leu | gtc<br>Val | aac<br>Asn | ctc<br>Leu | aaa<br>Lys | att<br>Ile | cct<br>Pro | 2841 |
| 920 925 930     |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| ctc<br>Leu      | ctg<br>Leu | tat<br>Tyr | gat<br>Asp | gct<br>Ala | gaa<br>Glu | att<br>Ile | cac<br>His | tta<br>Leu | aca<br>Thr | aga<br>Arg | tct<br>Ser | acc<br>Thr | aac<br>Asn | ata<br>Ile | aat<br>Asn | 2889 |
| 935 940 945     |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| ttt<br>Phe      | tat<br>Tyr | gaa<br>Glu | atc<br>Ile | tct<br>Ser | tcg<br>Ser | gat<br>Asp | ggg<br>Gly | aat<br>Asn | gtt<br>Val | cct<br>Pro | tca<br>Ser | atc<br>Ile | gtg<br>Val | cac<br>His | agt<br>Ser | 2937 |
| 950 955 960     |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| ttt<br>Phe      | gaa<br>Glu | gat<br>Asp | gtt<br>Val | ggt<br>Gly | cca<br>Pro | aaa<br>Lys | ttc<br>Phe | atc<br>Ile | ttc<br>Phe | tcc<br>Ser | ctg<br>Leu | aag<br>Lys | gta<br>Val | aca<br>Thr | aca<br>Thr | 2985 |
| 965 970 975     |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| gga<br>Gly      | agt<br>Ser | gtt<br>Val | cca<br>Pro | gta<br>Val | agc<br>Ser | atg<br>Met | gca<br>Ala | act<br>Thr | gta<br>Val | atc<br>Ile | atc<br>Ile | cac<br>His | atc<br>Ile | cct<br>Pro | cag<br>Gln | 3033 |
| 980 985 990 995 |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| tat<br>Tyr      | acc<br>Thr | aaa<br>Lys | gaa<br>Glu | aag<br>Lys | aac<br>Asn | cca<br>Pro | ctg<br>Leu | atg<br>Met | tac<br>Tyr | cta<br>Leu | act<br>Thr | ggg<br>Gly | gtg<br>Val | caa<br>Gln |            | 3078 |
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| aca<br>Thr      | gac<br>Asp | aag<br>Lys | gct<br>Ala | ggt<br>Gly | gac<br>Asp | atc<br>Ile | agt<br>Ser | tgt<br>Cys | aat<br>Asn | gca<br>Ala | gat<br>Asp | atc<br>Ile | aat<br>Asn | cca<br>Pro |            | 3123 |
| 1015 1020 1025  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| ctg<br>Leu      | aaa<br>Lys | ata<br>Ile | gga<br>Gly | caa<br>Gln | aca<br>Thr | tct<br>Ser | tct<br>Ser | tct<br>Ser | gta<br>Val | tct<br>Ser | ttc<br>Phe | aaa<br>Lys | agt<br>Ser | gaa<br>Glu |            | 3168 |
| 1030 1035 1040  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| aat<br>Asn      | ttc<br>Phe | agg<br>Arg | cac<br>His | acc<br>Thr | aaa<br>Lys | gaa<br>Glu | ttg<br>Leu | aac<br>Asn | tgc<br>Cys | aga<br>Arg | act<br>Thr | gct<br>Ala | tcc<br>Ser | tgt<br>Cys |            | 3213 |
| 1045 1050 1055  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| agt<br>Ser      | aat<br>Asn | gtt<br>Val | acc<br>Thr | tgc<br>Cys | tgg<br>Trp | ttg<br>Leu | aaa<br>Lys | gac<br>Asp | gtt<br>Val | cac<br>His | atg<br>Met | aaa<br>Lys | gga<br>Gly | gaa<br>Glu |            | 3258 |
| 1060 1065 1070  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| tac<br>Tyr      | ttt<br>Phe | gtt<br>Val | aat<br>Asn | gtg<br>Val | act<br>Thr | acc<br>Thr | aga<br>Arg | att<br>Ile | tgg<br>Trp | aac<br>Asn | ggg<br>Gly | act<br>Thr | ttc<br>Phe | gca<br>Ala |            | 3303 |
| 1075 1080 1085  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| tca<br>Ser      | tca<br>Ser | acg<br>Thr | ttc<br>Phe | cag<br>Gln | aca<br>Thr | gta<br>Val | cag<br>Gln | cta<br>Leu | acg<br>Thr | gca<br>Ala | gct<br>Ala | gca<br>Ala | gaa<br>Glu | atc<br>Ile |            | 3348 |
| 1090 1095 1100  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| aac<br>Asn      | acc<br>Thr | tat<br>Tyr | aac<br>Asn | cct<br>Pro | gag<br>Glu | ata<br>Ile | tat<br>Tyr | gtg<br>Val | att<br>Ile | gaa<br>Glu | gat<br>Asp | aac<br>Asn | act<br>Thr | gtt<br>Val |            | 3393 |
| 1105 1110 1115  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |

|                        |                           |                       |      |
|------------------------|---------------------------|-----------------------|------|
| acg att ccc ctg atg    | ata atg aaa cct gat       | gag aaa gcc gaa gta   | 3438 |
| Thr Ile Pro Leu Met    | Ile Met Lys Pro Asp       | Glu Lys Ala Glu Val   |      |
| 1120                   | 1125                      | 1130                  |      |
| cca aca gga gtt ata    | ata gga agt ata att       | gct gga atc ctt ttg   | 3483 |
| Pro Thr Gly Val Ile    | Ile Gly Ser Ile Ile       | Ala Gly Ile Leu Leu   |      |
| 1135                   | 1140                      | 1145                  |      |
| ctg tta gct ctg gtt    | gca att tta tgg aag       | ctc ggc ttc ttc aaa   | 3528 |
| Leu Leu Ala Leu Val    | Ala Ile Leu Trp Lys       | Leu Gly Phe Phe Lys   |      |
| 1150                   | 1155                      | 1160                  |      |
| aga aaa tat gaa aag    | atg acc aaa aat cca       | gat gag att gat gag   | 3573 |
| Arg Lys Tyr Glu Lys    | Met Thr Lys Asn Pro       | Asp Glu Ile Asp Glu   |      |
| 1165                   | 1170                      | 1175                  |      |
| acc aca gag ctc agt    | agc tgaaccagca gacctacctg | cagtgggaac            | 3621 |
| Thr Thr Glu Leu Ser    | Ser                       |                       |      |
| 1180                   |                           |                       |      |
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| tttggatgaa gaaattgtgg  | gggggtggggg aggtgcgggg    | ggcaggtagg gaaataatag | 3801 |
| ggaaaatacc tattttatat  | gatgggggaa aaaaagtaat     | ctttaaactg gctggcccag | 3861 |
| agtttacatt ctaatttgca  | ttgtgtcaga aacatgaaat     | gcttccaagc atgacaactt | 3921 |
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Ala Phe Gly Trp Ser Gly Thr Ile Val Gln Lys Thr Ser His Gly His  
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Leu Ile Phe Pro Lys Gln Ala Phe Asp Gln Ile Leu Gln Asp Arg Asn  
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His Ser Ser Tyr Leu Gly Tyr Ser Val Ala Ala Ile Ser Thr Gly Glu  
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Ser Thr His Phe Val Ala Gly Ala Pro Arg Ala Asn Tyr Thr Gly Gln  
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Ser Val Asp Val Asp Lys Asp Thr Ile Thr Asp Val Leu Leu Val Gly  
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Gly Pro Glu Gly Ile Glu Asn Thr Arg Phe Gly Ser Ala Ile Ala Ala  
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Ala Gln Ile Ile Leu Lys Leu Cys Phe Ser Ala Lys Phe Arg Pro Thr  
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Pro Ala Leu Glu Ala Tyr Ser Glu Thr Ala Lys Val Phe Ser Ile Pro  
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